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ALIGNMENTS

; TOPOLOGY: linear US-08-961-083-1 Sequence 1, Application US/08961083 Patent No. 6159469 TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: GENERAL INFORMATION: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: COMPUTER: HP Vectra 48 OPERATING SYSTEM: MSDO: SOFTWARE: ASCII Text CURRENT APPLICATION DATA: ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Anders TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 COMPUTER READABLE FORM: TITLE OF INVENTION: NUMBER OF SEQUENCES: SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS: LENGTH: 1999 base pairs TYPE: nucleic acid STRANDEDNESS: double APPLICATION NUMBER: FILING DATE: STREET: 9410 Ke CITY: Rockville REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER: MEDIUM TYPE: Diskette, Maryland E: Human Genome Scien 9410 Key West Avenue Choi et. HP Vectra 486/33 Genome Sciences, Inc. Streptococcus: 452 MSDOS version US/08/961,083 36,373 PB340P2 pneumoniae Antigens and Vaccines

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Sequence 5, Application U
Patent No. 6027906
Patent No. 6027906
GENERAL INFORMATION:
APPLICANT: Balganesh,
APPLICANT: Town, Chri
TITLE OF INVENTION: N
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS
ADDRESSEE: White &
STREET: 1155 Avenue

ADDRESS: Avenue

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FILING DATE: 2*
ATTORNEY/AGENT INFORMATION.

NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 354-8113
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2049 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucless: double
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US-08-481-435-5
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Best Local Similarity
Matches 1988; Conservat
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LOCATION:
FEATURE:
NAME/KEY:
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IMMEDIATE SOURCE:
LIBRARY: PCR cloning
CLONE: pARC 0512 Soluble
FEATURE:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Ne
COUNTRY:
ZIP: 1003
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                                                                                                                                                                                                                                                                   Sequence 3, Application US/08245511 Patent No. 5928900 GENERAL INFORMATION:
                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,511
FILING DATE: 18 MAY-1994
CLASSIFICATION: 424
                                                                                                                                                                                               APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED
TITLE OF INVENTION: ACELLULAR VACCINES
NUMBER OF SEQUENCES: 58
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APPLICATION NUMBER: 1
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STREET: 411 Hackensack A
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
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ADDRESSEE: Klauber & Jackson
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Best Local S
Matches 946
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SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDENESS: both
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069 (
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELLERAX: 201 343-1684
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CLONE: SPRU42
FEATURE:
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STRAIN: R
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 ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCCTGCTTACATGGA
                                                             AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCCAAGACCGCCGAAACTTGGTCTT
                                                                                  AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCCAAGACCGCCGAAACTTGGTCTT
                                                                                                      GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA
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Pred. No. 1.9
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1.9e-278;
les 3;
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US-08-600-993A-3
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                                                                                            MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,993A
FILLING DATE: 1-MAR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/245,511
FILLING DATE: 18-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILLING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069 U
TELECOMMUNICATION INFORMATION:
TELEPAX: 201 487-5800
TELEPAX: 201 487-580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                           SEQUENCE CHARACTERISTICS
LENGTH: 960 base pai
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
MOLECULE TYPE: DNA (ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: BACTERIAL EXPORTED TITLE OF INVENTION: ACELLULAR VACCINES NUMBER OF SEQUENCES: 59
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CITY: Ha
STATE: N
COUNTRY:
ZIP: 076
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CLONE: SPRU42
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STRAIN: F
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nes 946; Conserv
                        TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT
                                                                                                           ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA 660
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           TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT
                                                         AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATAT
                                                                                                                                   TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAACAGGCTATAACCTACTCAC
                                                                                                                                                                                                             ATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC
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Pred. No. 1.9e-278;
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                                                                                                                             Matches
                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: OUELLETTE APPLICANT: ROY, Paul TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                               3498
 3438
                                                                                                                                                                                                                                          MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 9100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: 08/526,840
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                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                             TAAATTAATTGGCGAAGTGGGTGAGCAACGCCGTATTCCAGTGAAATTAGCCGATGTGCC
                                                                                           TCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAATGCCCAAGCTAATGATATTCC
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NO. 5994066
                              CACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCATCGCTTCTTCGACCACAGGGG
ACAACGCTTAATTGACGCATTTTTAGCGACGGAAGACAGTCGTTTTTACGATCATCACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTTTCCTTCGGAATTAACCAAGCAGTAGAAACAAACCGCGACTGGGGA 949
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                                                                                                                                                                                                                                                                                                                                                                                                                           PAGENT ATTEMPT OF THE PAGE NOT NOT MEET: 35,433
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                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-SEP-1995
                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-SPECIFIC AND UNIVERSAL DNA
PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
                                                                                                                                            5.9%;
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                                                                                                                          Score 117.2; DB 2;
Pred. No. 2e-25;
0; Mismatches 333;
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: OUELLETTE, MARC
APPLICANT: ROY, Paul H.
TITLE OF INVENTION: SPECIFIC
TITLE OF INVENTION: AMPLIFIC
TITLE OF INVENTION: COMMON B
TITLE OF INVENTION: FROM CLI
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                    SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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ADDRESSEE: QUARLES & BRADY
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CITY: Milwaukee
STATE: Wisconsii
                                                                  APPLICATION NUMBER: FILING DATE: 11-SEI
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AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE
FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ....
177
                                                                                                                      Release #1.0, Version
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Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
 2847
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ORIGINAL SOURCE:
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GGTGCGTCGTTTTGGCGAAGAAAATGCTTACACC 2814
                               CATCAATCAAGTTGAAGAAGAAACAGGCTATAAC 712
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                                                               TCACGGCGCAAAATTTGAATTTCGAGCCGATTATGTCACTGAAATGGTGCGTCAAGAAAT
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Pred. No. 2e-25
0; Mismatches
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Best Local S
Matches 290
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                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 01-JUL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2487 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: SE 9 FILING DATE: 24-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 01-JUL-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Balganesh, Tanja
APPLICANT: Town, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
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                                             140 TTACGTTGGATCAAATCCCACCGGAGATGGTGAAAGCCTTTATCGCGACAGAAGACAGCC
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                                                                                                                                                              Local Similarity
nes 290; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 10-JUI
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                                                                          63
                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                   STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Sterner, Richard REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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GCTTCTTCGACCACGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAATC
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                                                                     CCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCATC 122
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SYSTEM: PC-DOS/MS-DOS
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US-08-771-716-1
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                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hoskins, Joann
APPLICANT: Jaskunas, S.Richard
APPLICANT: Skatrud, Paul L.
TITLE OF INVENTION: Monofunctional Glycosyltransferase
TITLE OF INVENTION: Gene of Staphylococcus Aureus
NUMBER OF SEQUENCES: 3
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                LENGTH:
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nucleic
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Patent No. 592254
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APPLICANT: Peery, Robert B.
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                      APPLICANT: Hoskins, JoAnn
APPLICANT: Jaskunas, S.Richard
APPLICANT: Skatrud, Paul L.
TITLE OF INVENTION: Monofunctional Glycosyltransferase
TITLE OF INVENTION: Gene of Staphylococcus Aureus
ATTORNEY/AGENT INFORMATION:
                                                           CURRENT APPLICATION DATA:
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HYPOTHETICAL: NO
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                                                                                                                                                                              STREET: Lilly Corp
CITY: Indianapolis
STATE: Indiana
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                           APPLICATION NUMBER: FILING DATE:
                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
              CLASSIFICATION:
                                                                       SOFTWARE:
                                                                                                                                                    ZIP: 46285
                                                                                                                                                               COUNTRY:
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Local Similarity 49.98;
                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                           Lilly Corporate Center
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                                                                       PatentIn Release #1.0,
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Pred. No. 3.4e-09;
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NAME: Webster, Thomas REGISTRATION NUMBER: 1

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                                                                                                                                                                                                                                                                                      Sequence 1, Application Patent No. 6143868
GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT:
APPLICANT:
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TELECOMMUNICATION: INFORMATION:
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LENGTH: 807 base pairs
TYPE: nucleic acid
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                        TITLE OF INVENTION: Monofunctional Glycosyltransferase TITLE OF INVENTION: of Staphylococcus Aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                                                                                          ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center CITY: Indianapolis
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                              COUNTRY:
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Jaskunas, S.Richard
Skatrud, Paul L.
                                                                              U.S.
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Pred. No. 3.4e-09;
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US-09-057-720A-3

Sequence 3, Application US/09057720A

Patent No. 143868
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Best Local Similarity
Matches 191; Conserv
                                                                                                                               GENERAL INFORMATION:
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                                         APPLICANT: Jaskunas,
APPLICANT: Skatrud, E
TITLE OF INVENTION: N
TITLE OF INVENTION: C
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NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,
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LENGTH: 807 base pairs
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TELECOMMUNICATION INFORMATION:
                                                                                   APPLICANT: Peery, Robert B.
APPLICANT: Hoskins, Joann
APPLICANT: Jaskunas, S.Richard
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HYPOTHETICAL: NO
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                           NUMBER OF SEQUENCES:
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                          Monofunctional Glycosyltransferase of Staphylococcus Aureus
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Pred. No. 3.4e-09;
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Indianapolis

Lilly Corporate Center

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Best Local S
Matches 130
                                                         Sequence 1, Application Patent No. 5789202
               GENERAL INFORMATION:
APPLICANT: Hoskin
APPLICANT: Jaskun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
 APPLICANT:
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HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
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mes 130; Conserv
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STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/057,720A
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Rockey, Pamela K.
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317-17 NO: 3:
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                                                                       US/08731716
               S. Richard
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Pred. No. 3.4e-09;
1; Mismatches 183;
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Best Local S
Matches 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: lir
MOLECULE TYPE:
HYPOTHETICAL: N
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LENGTH: 2193 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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APPLICANT: No. 5789202ris, Franklin H.
TITLE OF INVENTION: Penicillin Binding Protein From
TITLE OF INVENTION: Streptococcus Pneumoniae
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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365 TACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAAAGAC 424
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release "
                                                                                                                                                                                                                                                                                                                                                                                                                     283 ATTTTTGACCGTGAAGAAAAAGAGCTGGTGCCTTGTCTGGTCAAAAGGGAACCTATGTT 342
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                                                      TTAGAATTAAGCAAAAATATAGTAAGGAGCAAATTCTAACCATGTACCTTAACAACGCT
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Pred. No. 3.4e-07;
0; Mismatches 446;
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              TELEPHONE: 317-276-33
INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                             TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosteck, Paul R. Jr.
APPLICANT: No. 5789202ris, Franklin H.
TITLE OF INVENTION: Penicillin Binding Protein
TITLE OF INVENTION: Streptococcus Pneumoniae
NUMBER OF SEQUENCES: 3
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                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                 REGISTRATION NUMBER: 39
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                   CITY: Indianapolis
                                                                                                    NAME: Webster, Thomas
                                                                                                                                                     FILING DATE:
                                                                                                                                                                       APPLICATION NUMBER:
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CHARACTERISTICS:
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Rockey, Pamela K.
Zhao, Genshi
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Best Local Sim
Matches 270;
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MOLECULE TYPE:
HYPOTHETICAL: 1
1105 GGAAGUGUAGCUCU
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STRANDEDNESS: single
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                               ACCATTGTTGATGT
                                                                                             GATATTTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCT
                                                                                                                                                               CTCACAACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGG
                                                                                                                                                                                                                                  TACCTCAAGGAAGTCATCAATCAAGTTG-----AAGAAGAAACAGGCTATAACCTA 715
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                                                              AUUGUUUAUGAAAACACAUCGCUAUUUCCGAGGGCAGAGGAUGGAACGUUUGCUCAAUCA 1104
                                                                                                                                GUCAAUAAUGGCUACCGCAUUUACACAGAGCUGGACCAAAACUACCAAGCAAAUAUGCAG
                                                                                                                                                                                                  UAUUUUGAUGCGGUGGUUAAUGAAGCUGUUUCCAAGUAUAAUCUAACAGAGGAAGAGAUU
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Pred. No. 3.4e-07;
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GENERAL INFORMATION:

APPLICANT: STRAUSS, ANDREAS

APPLICANT: THUMM, GUNTHER

APPLICANT: POHLMER, JOHANNES

APPLICANT: GOTZ, FRIEDRICH

TITLE OF INVENTION: METHOD FOR IDENTIFYING A :

FILE REFERENCE: 10496/P65266US0

CURRENT APPLICATION NUMBER: US/09/508,542

CURRENT FILING DATE: 2000-05-16

PRIOR APPLICATION NUMBER: PCT/EP98/06136

PRIOR APPLICATION NUMBER: 97 116 841.4

PRIOR FILING DATE: 1997-09-27

PRIOR APPLICATION NUMBER: 97 116 841.4

PRIOR FILING DATE: 1997-09-27

PRIOR APPLICATION NUMBER: 97 116 841.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-060-756-206
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Patent NO. 6183957
GEMERRAL INFORMATION:
APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Buchrie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 17, Application US/09508542 Patent No. 6339174
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Best Local Similarity
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CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 206
SEQ ID NO 206
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247 gcccggcggaacgtggtcct 266
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Search completed: August Job time: 27634 sec

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LENGTH: 1474

TYPE: DNA
ORGANISM: Staphylococcus carnosus
FEATURE:
NAME/KEY: modified_base
LOCATION: (1)..(1474)
OTHER INFORMATION: "n" represents a,
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Best Local Similarity 50.4%;
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Listing first 45 summaries
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79: /cgn2_6/ptodata/2/
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ω	Result No
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Sequence 3, Applisequence 139, App Sequence 139, App Sequence 6631, Ap Sequence 6631, Ap Sequence 6631, Ap Sequence 6631, Ap Sequence 1534, Ap Sequence 217, App Sequence 217, App Sequence 2013, Ap Sequence 2013, Ap Sequence 495, App Sequence 410,	Description Sequence 1, Appli Sequence 1 Appli Sequence 11, Appli Sequence 115, Appl Sequence 1112, Appli Sequence 1112, Appli Sequence 9325, Ap Sequence 9325, Ap Sequence 9325, Ap Sequence 596, Appli Sequence 596, Appli

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LENGTH: 1999 base pair
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ II
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Best Local Similarity
Matches 1999; Conserv
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GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Scier
                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: CUNKnown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/961,083
FILING DATE: 0CT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
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MEDIUM TYPE: Diskette, 3:50 inch
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version
SOFTWARE: ASCII Text
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CITY: Rockville
STATE: Maryland
COUNTRY: USA
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6 US-09-63-779-1038

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7 US-09-620-608-1543

7 US-09-328-352-2090

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                      APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pr
NUMBER OF SEQUENCES 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Science
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
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Best Local Similarity
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FILING DATE: «Unknown»
APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-197
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
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ATCTGAAATGAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC
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STRANDEDNESS: double
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OPERATING SYSTEM: MSDOS ve
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TOPOLOGY: linear; SEQUENCE DESCRIPTION: US-09-765-272-1
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US-09-765-272-1
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; GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1999 base pairs
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ADDRESSE: Human Genome Scien
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Choi et. al. TITLE OF INVENTION: Streptococcus
                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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               Similarity
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                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
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                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                  NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Diskette, 3.50 inch,
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.
SOFTWARE: ASCII Text
                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
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US-60-029-960-81/c
; Sequence 81, Application US/
; GENERAL INFORMATION:
APPLICANT: Charles Kunsc
; TITLE OF INVENTION: Stre
; NUMBER OF SEQUENCES: 164
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genom
; STREET: 9410 Key West
; CITY: Rockville

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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 81:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETLE, 3
COMPUTER: HP Vectra 486,
OPERATING SYSTEM: MSDOS
SOFTMARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION: DATA:
APPLICATION: DATA:
PRIOR APPLICATION DATA:
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             ATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAAGCAGTCAATAC
                                              AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT
                                                                                             AGACCTCAATAATTTAAGTTTACCTCAGTTAGCCTTGCCTGGCAGTGCCTCAGGCACC
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                                  AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT
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100.0%; ilarity 100.0%; Conservative
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            GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT
                                                          GACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATACGCGTAAATATTCAAT
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US-08-961-527-145
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                                                                                                               REFERENCE/DOCKET NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 10711 base pairs
TYPE: nucleic acid
STRANDEDNESS: 2007.
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                           Query Match
Best Local Sim
Matches 1999;
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                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
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                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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NUMBER OF SEQUENCES:
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CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                               NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                      FILING DATE:
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; Sequence 1312, Application US/0958; GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm ei TITLE OF INVENTION: Nucleic Acid TITLE OF INVENTION: Pneumoniae for FILE REFERENCE: PATHOO-07A

CURRENT APPLICATION NUMBER: US/09; CURRENT FILING DATE: 2000-05-26
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PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: US 60/

PRIOR APPLICATION NUMBER: US 60/

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 1312

LENGTH: 2160

TYPE: DNA

ORGANISM: Streptococcus pneumo
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US-09-107-433-1102
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Sequence 1102, Application:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCCCCUS I
THERAPEUTICS
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                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                             NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489 REFERENCE/DOCKET NUMBER: GTC-0 TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                           FEATURE:
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LENGTH: 2166 base pairs
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CORRESPONDENCE ADDRESS:
                                     TAAAATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGCTCAA
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ZIP: 0235
                                                                                                                                                                                NAME/KEY:
LOCATION:
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FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid STRANDEDNESS: double
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STATE: Massachusetts
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                                                                                         Conservative
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RESULT 8
PCT US02-03987-9325
Sequence 9325, Application PC/TUS0203987
GENERAL INFORMATION:
APPLICANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the TITLE OF INVENTION: Methods for Identifying the TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028VPC
CURRENT APPLICATION NUMBER: PCT/US02/03987
CURRENT FILING DATE: 2002-02-02
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0 the

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Best Local Similarity
Matches 1988; Conser
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LOCATION: (1)...(2160)
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Pred. No. 0;
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TITLE OF INVENTION: Identification of Es:
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITAR.011A
CURRENT APPLICATION NUMBER: US/09/815,24:
CURRENT FILING DATE: 2001-03-21
PRIOR PPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PRILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
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ORGANISM: Streptococcus p
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(2160)
S-09-815-242-9325
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Best Local Similarity
Matches 1988; Conserv
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GENERAL INFORM
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APPLICANT:
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APPLICANT: Ohlsen, K
APPLICANT: Zyskind,
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INFORMATION:
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Zyskind, Judith W.
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TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT
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638 540 698 600 758 660 818

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1080 1238 1140 1298 1200

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PRIOR APPLICATION NUMBER: 2002-02-08
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4
SEQ ID NO 9325
LENGTH: 2160
TYPE: DNA
ORGANTO:
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APPLICANT: Carr, Grant J.
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                                                                                    APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
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ORGANISM: Streptococcus
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Boone, Charles
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Zyskind, Judith W.
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                     TGTTTCCTTCGGAATTAACCAAGCAGTAGAAACAAACCGCGACTGGGGGATCAACTATGAA
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APPLICANT: LAGACE, ROBERT E.
APPLICANT: LAGACE, NETL C.
APPLICANT: HANN, AMY L.
APPLICANT: HANN, AMY L.
APPLICANT: HEATH, JOE D.
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
THEREOF AND USES: 797

CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 31/4 PORTER DRIVE
CITY: PALO ALTO
STREET: 31/4 PORTER DRIVE
COMPUTER: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HEADABLE FORM:
COMPUTER: HEADABLE FORM:
APPLICATION NUMBER: US/60/061,998
FILING DATE:
APPLICATION NUMBER: US/60/061,998
FILING DATE:
CLASSIFICATION NUMBER: DM 0006-2P
TELEPHONE: (650) 845-4166
INFORMANION: 596:
SEOURCE CHARACTERISTICS:
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US-60-061-998-596
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US-60-661-998-596/c
; Sequence 596, Application US/60061998
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 1988; Conserv
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
CLONE: SPN1C601
  9478
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TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA 120
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Pred. No. 0;
0; Mismatches
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RESULT 12
US-60-068-175-596/c
US-60-068-175-596/c
; Sequence 596, Application US/60068175
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert E.
; APPLICANT: Corley, Neil C.
; APPLICANT: Corley, Frank D.
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                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for W
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                APPLICANT: Lagace, Robert E.
APPLICANT: Corley, Neil C.
APPLICANT: Russo, Frank D.
APPLICANT: Hann, Amy L.
APPLICANT: Heath, Joe D.
APPLICANT: Finney, Gregory L.
APPLICANT: MYENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE
TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF
NUMBER OF SEQUENCES: 1175
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STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
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APPLICATION NUMBER: FILING DATE: HEREWI CLASSIFICATION:
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US-60-068-175-596
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INFORMATION FOR SEQ ID NO: 596:
SEQUENCE CHARACTERISTICS:
LENGTH: 9845 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: genomic DNA
IMMEDIATE SOURCE:
CLOURE: SPN2C598
-60-068-175-566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 81.6%;
Best Local Similarity 88.8%;
Matches 1776; Conservative
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NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REGISTRATION NUMBER: PM-0009-2
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                                                                                                  ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCT-GCTTACATGG
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             CAACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAAACATCTGTGGGATA
                                    ATAATTACCTCAAGGAGGTCATCAATCAAGTAGAACAAGAAACTGGCTATAACCTTCTAA
                                                                                      ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCCTGGCTTACATGG
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Score 1631.2;
Pred. No. 0;
0; Mismatches
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934 GCCCAATATGGACTGAACCCTCTACTCAACAATCCTCAACAGCTGAAAGTTCAAGCTCAT 7875	Db 79
994 ACTGGACGATGCCAGACGGACTTTTCAGAAACGGGGAATTTGTATTCAAAAATGGAGCTC 793	ъ 79
740 ATTGGAATATACCAGAGGGGCTCTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTC 179	17
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80 TCGCTGCCAAAGTTTACCGCTCTATGATGACCTACCTGTCTGAAGGAAG	_
\circ	80
20 TGGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTAC	6
	81
60	15
	82
00 CTCAGGCTGGTAAAACAGGAACCTCTAACTATACAGACGAGGAAATTGAAAACCACATC	Qy 15
294 ACATGATGAAAACAGTCTTGACTTATGGAACTGGGGGGTGGAGCCTATCTTCCTTGGCTTC 8235	82
40 ACATGATGAAAACAGTCTTGACTTATGGAACTGGACGAAATGCCTATCTTGCTTG	Оу 14
354 AAGAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGACGCG 8295	83
80 AAGAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACC	w
414 GTGGCACTTACTATAAACCAATGTATATCCATAAAGTCGTCTTCAGTGGAAGTAAAA 8355	84
20 GTGGAACTTACTATAAACCAATGTATATCCATAAAGTCGTCTTTAGTGATGGGAG	ω
474 ATAAACAATACGGAGCAAGTAGTGAAAAAATGGCTGCTGCTTATGCTGCCTTTTGCAAATG 8415	Db 84
60 ACAAAAAATATGGAGCAAGTAGTGAAAAGATGGCTGCTGCTTACGCTGCCTTTGG	12
534 GTATCGACTATCCAAGCATGCATTATGCAAACGCCATTTCAAGTAATACAACAGAATCTA 8475	85
00 GAATCGACTACCCAAGTATTCACTACTCAAATGCCATTTCAAGTAACACAACCC	12
594 CCGTTGAGACTTTGAATAAGGTCGGTCTAGATAGAGCTAAAACCTTCCTT	85
40 CCGTGGAAACTCTAAACAAGGTCGGACTCAACCGCGCCAAGACTTTCCTAAATGGTCTA	$\mathbf{\dot{\mu}}$
654 GAGCATATTTCGGTAATATTACTCTGCAATATGCTCTTCAACAATCACGAAATGTCACAG 8595	86
80 GGGGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAACAATCGCGAAACGTCCC	10
714 TGGTTAATGATATTCCTTATAACTATCCGGGAACAAGCACACCTGTCTACAACTGGGATA 8655	87
20 TCGTTCACGATGAGCCCTATAACTACCCTGGGACAAATACTCCTGTTTA	Qy 10
774 AACCAATCACCGATTATGCACCTGCCATAGAATACGGTGTTTATGATTCCACTGCAACTA 8715	Db 87
60 AACCGATCACAGACTATGC	9
34 ACGTTTCATTTGGTACCAACCAAGCTGTGGAAACCAATCGTGACTGGGGTTCTGC	Db 88
0 ATGTTTCCTTCGGAATTAACCAAGCAGTAGAAACAAACCGCGACTGGGGATC	
894 TCGTAGATGTTTCAAATGGTAAAGTCATCGCCCAACTTGGAGCTCGTCACCAAGCAAG	8.8
40 TTGTTGATGTTTCTAACGGTAAAGTCATTGCCCAGCTAGGAGCACGCCATCAGT	co
54 TCTACE	89
80 TTTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTA	7
014 CTACTGGGATGGATGTTTACACAAATGTAGACCAAGAAGCTCAAAAAACATCTGTGGGATA 8955	Db 90

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Qy
                                                                                                                         ; NAME/KEY:
; LOCATION:
US-08-116-541-3
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US-08-116-541-3
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPAX: 201 343-1684
TELEFAX: 133521
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08116541
GENERAL INFORMATION:
APPLICANT: Masure, H. Robert
APPLICANT: Pearce, Barbara J.
APPLICANT: Toumanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 45
                                   Query Match
Best Local Similarity
Matches 946; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, VG
COURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSEE: Klauber &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                               FEATURE:
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HYPOTHETICAL:
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                                                                                                                                                                                           IMMEDIATE SOURCE:
CLONE: SPRU42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US FILING DATE: 19930901
                                                                                                                                                                                                                               STRAIN:
                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
 TAAAATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAA 60
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99.7%;
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                                   Score 944.2; DB
Pred. No. 1e-256;
Mismatches
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                                   Indels
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RESULT 14 PCT-US97-14436-139

Sequence 139, Application PC/TUS9714436 GENERAL INFORMATION:

APPLICANT:
APPLICANT:
APPLICANT:

Black, Michael Hodgson, John Knowles, David Lonetto, Michael

APPLICANT:

Nicholas,

Richard

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                 901 TGTTTCCTTCGGAATTAACCAAGCAGTAGAAACAAACCGCGACTGGGGA 949
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                                                                         TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT 840
                                                                                                              AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAAACATCTGTGGGATAT
                                                                                                                                                  TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAGTTGAC 240
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; TOPOLOGY: 1i;
; MOLECULE TYPE:
PCT-US97-14436-139
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CORRESPONDENCE ADDRESS:
ANDRESSEE: SmithKline Beecham Corporation
ANDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for WI
CURRENT APPLICATION UNMBER: PCT,
APPLICATION NUMBER: PCT,
FILING DATE: 15-AUG-1997
                                                                                                                                                                                                             1354
                                                                                                                                                                                                                                                                                                               1234 CATTTCAAGTAACACAACCGAATCAGACAAAAAATATGTGGAGCAAGTAGTGAAAAGATGGC 1293
                                                                                                                                                                                                                                                                                                                                                                           1174 CGCCAAGACTTTCCTAAATGGTCTAGGAATCGACTACCCAAGTATTCACTACTCAAATGC
1414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                                                                                                                                                                                                                                                       1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/0:
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                 181
                                                                                                                                                                                                                                          121
                                                            301
                                                                                                                      241
                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2172 base pairs TYPE: nucleic acid STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                       TGCTGCTTACGCTGCCTTTGCAAATGGTGGAACTTACTATAAACCAATGTATATCCATAA: 1353
                                                                                                                   AGTCGTCTTTAGTGATGGGAGTGAAAAAGAGTTCTCTAATGTCGGAACTCGTGCCATGAA
                                                         ACG-AAATGCCTATCTTGCCTTGGCTCCCTCAGGCTGGTAAAACAGGAACCTCTAACTATA 1532
                                                                                                                                                                                                           AGTCGTCTTTAGTGATGGGAGTGAAAAAGAGTTCTCTAATGTCGGAACTCGTGCCATGAA 1413
                                                                                                                                                                                                                                                                                                 CATTTCAAGTAACACAACCGAATCAGACAAAAAATATGGAGCAAGTAGTGAAAAAGATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic DNA
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) for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                 40.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 808.6; DB 1;
Pred. No. 5.1e-218;
0; Mismatches 4;
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US-08-911-503-139
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Sequence 139, Application:
GENERAL INFORMATION:
GENERAL TOANT: Black, Michael
TOANT TOANT: John
                                                                                                                                                              PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 60/024,022

FILING DATE: 16-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Gimmi, Edward R

REGISTRATION NUMBER: 38,891
                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                            REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: NOVEL PROKARYOTIC POLYNUCLEOTIDES,
TITLE OF INVENTION: POLYPEPTIDES AND THEIR USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
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Lonetto, Michael
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Search completed: August 11, Job time: 9723 sec

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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

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4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

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US-10-128-844-2

US-09-673-476-206

US-09-673-476-626

US-09-673-476-438

7 US-10-179-131-3144

US-10-179-131-3015

US-09-673-476-438

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US-10-179-131-1548

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US-10-179-131-385

US-10-179-131-385

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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	sequence
3751, Ap	86, Appl	25, Appl	25, Appl	25, Appl	25, Appl	25, Appl	25, Appl	309095,	82144, A	1603, Ap	185, App	2414, Ap	1, Appli	4136, Ap	15709, A	99, Appl	148124,	54, Appl	ddw '110

ALIGNMENTS

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RESULT 1
US-08-961-083-1
; SEQUENCE DESCRIPTION: SEQ ID US-08-961-083-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08961083 GENERAL INFORMATION:
                                                                                                        TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1999 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: HP Vectra 48
                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                             APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Choi et. al. TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII Text
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                                            TOPOLOGY: linear
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                                ACCGATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTAT
                                                                              TGTTGATGTTTCTAACGGTAAAGTCATTGCCCAGCTAGGAGCACGCCATCAGTCAAGTAA
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APPLICANT: Kunsch et al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Scier
STREET: 9410 Key West Avenue

Sciences,

pneumoniae

Polynucleotides

and

Sequences

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RESULT 2
US-10-158-844-145/c
US-10-158-844-145/c
; Sequence 145, Application US/10158844
; GENERAL INFORMATION:
APPLICANT: KUNSCh et al.
TITLE OF INVENTION: Streptococcu:
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 9410 Key West Avenue
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 1999;
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INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
                          9287
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541 ATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC
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MEDIUM TYPE: CD-R

COMPUTER: Dell Latitude Pentium 3

OPERATING SYSTEM: Windows 98

SOFTWARE: ASCII Text

CURRENT APPLICATION NUMBER: US/10/158,844

FILING DATE: 03-Jun-2002

CLASSIFICATION: CURKNOWN>
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FILING DATE: 1997-10-30
APPLICATION NUMBER: US 60/029,960
FILING DATE: 1996-10-31
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                        AAACCAATATGACCCCTATTCACATCCAGAAGCCAGCCCAAGACCGCCGAAACTTGGTCTT
                                   AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT
                                                                           AGACCTCAATAATTTAAGTTTACCTCAGTTAGCCTTGCCTGGCAGGGAATGCCTCAGGCACC 480
                                                                                                                                                         GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA 420
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STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 10711 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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1680	GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT	1621	Qy
1620	GACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATACGCGTAAATATTCAAT	1561	Qy
8148		8207	Db
1560	TCAGGCTGGTAAAACAGGAACCTCTAACTATACAGACGAGGAAATTGAAAACCACATCAA	1501	Qy
8208		8267	Db
1500	CATGATGAAAACAGTCTTGACTTATGGAACTGGACGAAATGCCTATCTTGCTTG	1441	Qy
8268		8327	Db
1440	AGAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACGA	1381	Qy
8328		8387	Db
1380	TGGAACTTACTATAAACCAATGTATATCCATAAAGTCGTCTTTAGTGATGGGAGTGAAAA	1321	Qy
8388		8447	Db
1320	CAAAAATATGGAGCAAGTAGTGAAAAGATGGCTGCTTACGCTGCCTTTGCAAATGG	1261	Qy
8448		8507	Db
1260	AATCGACTACCCAAGTATTCACTACTCAAATGCCATTTCAAGTAACACAACCGAATCAGA	1201	Qy
8508		8567	Db
1200	CGTGGAAACTCTAAACAAGGTCGGACTCAACCGCGCCAAGACTTTCCTAAATGGTCTAGG	1141	Qy
8568		8627	Db
1140	GGGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAACAATCGCGAAACGTCCCAGC	1081	Qy
8628		8687	Db
1080	CGTTCACGATGAGCCCTATAACTACCCTGGGACAAATACTCCTGTTTATAACTGGGATAG	1021	Qy
8688		8747	Db
1020	ACCGATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTAT	961	Qy
8748		8807	Db
8088	TGTTTCCTTCGGAATTAACCAAGCAGTAGAAACAAACCGCGACTGGGGATCAACTATGAA	901	Qy
096		8867	Db
900	TGTTGATGTTTCTAACGGTAAAGTCATTGCCCAGCTAGGAGCACGCCATCAGTCAAGTAA	841 8927	Qy Db
840	TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT	781	Qy
8928		8987	Db
780	AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATAT	721	Qу
8988		9047	рь
720	TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAAACAGGCTATAACCTACTCAC	661	Qy
9048		9107	Db
660	ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA	601	. Qy
9108		9167	Db
9168		9227	Db

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APPLICANT: Obellette, Marc

APPLICANT: Roy, Paul H.

ITITLE OF INVENTION: Specific and Universal Probes and Amplification

TITLE OF INVENTION: Priners

TITLE OF INVENTION: Priners

TITLE OF INVENTION: to Rapidly Detect and Identify Common Bacterial

TITLE OF INVENTION: Pathogens and Antibiotic Resistance Genes from Clir

TITLE OF INVENTION: Specimens for Routine Diagnosis in Micro

FILE REFERENCE: 12287.31

CURRENT FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: 09/452,599

PRIOR APPLICATION NUMBER: 09/452,599

PRIOR FILING DATE: 1999-12-01

PRIOR APPLICATION NUMBER: 09/304,732

PRIOR FILING DATE: 1994-09-12

NUMBER OF SEQ ID NOS: 177
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TYPE: DNA
ORGANISM: Haemophilus
US-10-121-120-27
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APPLICANT: Bergeron, Michel G.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver.
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Local Similarity 50.3%;
hes 349; Conservative
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                GATTGATACCATCCGGTATCCTGGGAGCTTTCTTGCGCAATCTGCAAA---GCAATTCCCT
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                                                   ATTAGACCCTATCGGCATTGCCCGTGCATTGTTTGTCGCAGTGAGTAATGGCGGTGCATC
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Pred. No. 2.6e-
0; Mismatches
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS; FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 3719
LENGTH: 2370
TYPE: DNA
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US-09-540-209B-3719
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Best Local Similarity 46.9%;
Matches 261; Conservative
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                          TCACCCAACAGTTGATTAA-----GTTGACTTACTTTTCAACTTCGACTTCCGACCAGA 269
                                                                                                                                                                  TCGTTTCTATCGAAGACCATCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCC
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tttcacaacagctcgccaagcaattgtttacggacgaagttgccagaaatacgctgcagc 472
                                                                                                           TGGGAGCTTTCTT-----GCGCAATCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTC
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                                                                                                                                                                                                                                                                                          Score 59.2; DB 5;
Pred. No. 3.8e-06;
0; Mismatches 283;
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RESULT 5
US-10-158-844-2/c
Sequence 2, Application US/10158844;
GENERAL INFORMATION:
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                                                                 Matches 371;
                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: PB340P1D1 INFORMATION FOR SEQ ID NO: 2:
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                        S
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/961,527
FILING DATE: 1997-10-30
APPLICATION UMBER: US 60/029,960
FILING DATE: 1996-10-31
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 7571 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Streptococcus NUMBER OF SEQUENCES: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kunsch et al.
ATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAATGCC 64
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                                                                                     Similarity
                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/158,844
FILING DATE: 03-Jun-2002
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                           NAME: Hyman, Mark J. REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Maryland
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                                                                 Conservative
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                                                                                 2.9%;
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                                                             Score 57.8; DB 7;
Pred. No. 1.4e-05;
D; Mismatches 427;
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                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
               APPLICANT: BILLAULT, ALAIN

TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
TITLE OF INVENTION: WYCOBACTERIA.

TITLE OF INVENTION: WYCOBACTERIA.

FILE REFERENCE: 05394.0011-00000
CURRENT APPLICATION NUMBER: US/09/673,476
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: PCT/IB99/00740
PRIOR FILING DATE: 1999-04-16
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                          APPLICANT: COLE,
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  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                   206, Application
                                                                                                                                                                                                                                BUCHRIESER-BROSCH, ROLAND GORDON, STEPHEN
                                                                                                                                                                                                                                                                            STEWART
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  09/060,756
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1440

1500

664

PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: Patentin Ver. 2.2
SEQ ID NO 206
LENGTH: 428

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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-673-476-626
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; LOCATION: (280)
; OTHER INFORMATION: a, t, c or
US-09-673-476-206
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                                                             Query Match
Best Local Similarity
Matches 113; Conserv
                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. SEQ ID NO 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 626, Application US/09673476 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED TITLE OF INVENTION: DAA LIBRARY APPLICATION TO THE DETECTION OF TITLE OF INVENTION: MYCOBACTERIA.

FILE REFERENCE: 05394.0011-00000

CURRENT APPLICATION NUMBER: US/09/673,476

CURRENT FILING DATE: 2002-03-29

PRIOR APPLICATION NUMBER: PCT/IB99/00740

PRIOR FILING DATE: 1999-04-16
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/060,756
PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: COLE, STEWART APPLICANT: BUCHRIESER-BI APPLICANT: GORDON, STEPI APPLICANT: BILLAULT, ALJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                                                                               LENGTH: 363
326 ACCAAGCAAGAAATCTTGACCTACTATATAAAATAAGGTCTACATGTCTAATGGGAACTAT 385
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                                                               Conservative
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                                                             Score 51.8; DB 5;
Pred. No. 0.00023;
0; Mismatches 102;
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2.7e-05;
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US-10-179-131-2857
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US-10-179-131-3144
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                                                                                                                                                                                                                                         Sequence 2857, Application US/10179131 GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 10194
SEQ ID NO 3144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3144, Application US/10179131 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.2%;
Best Local Similarity 58.2%;
Matches 78; Conservative
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APPLICANT:
               APPLICANT: ZENG, QIANDONG
APPLICANT: GREENE, JONATHAN R.
TITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 2976-4031
CURRENT APPLICATION NUMBER: US/10/179,131
CURRENT FILING DATE: 2002-06-21
                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                      APPLICANT: HARE, ROBERTA S. APPLICANT: SHAW, KAREN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: GREENE, JONATHAN R.
TITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC ACIDS AND POLYPEPTIDES,
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 2976-4031
                                                                                                                                                 APPLICANT:
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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TYPE: DNA
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1864 AGATAGTTCAACCTTCACAGTCTAGCTCAACCACTCCAAGCACAAATAATAGTACGACTAC 1923
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1924 CAATCCTAACAATAATACGCAACAATCAAATACAACCCCTGATCAACAAAATCAGAATCC 1983
                                                                                                                                                                                                                                                                                                                                                                                                 1984 TCAACCAGCACAAC 1997
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NOLLING, JORK
ZENG, QIANDONG
                                                                                                                                                                                    SHIMER JR., GEORGE
                                                                                                                                               KESSLER, MARCO
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                                                                                                                                                                                                                                                                                                                                                            208
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Pred. No. 0.043;
0; Mismatches 56;
                                                                                             ACIDS
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                                                                                             AND POLYPEPTIDES,
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; OTHER INFORMATION: a,
US-09-673-476-438
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; ORGANISM: Candida albicans
US-10-179-131-2857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/060,756
PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PATENTIN VEr. 2.2
SEQ ID NO 438
LENGTH: 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 438, Application US/09673476 GENERAL INFORMATION:
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LENGTH: 1350
                                                                                                                         Best Local Similarity
                                                                                                                                          Query Match
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TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
TITLE OF INVENTION: MYCOBACTERIA.
FILE REFERENCE: 05394.0011-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/673,476
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: PCT/IB99/00740
PRIOR FILING DATE: 1999-04-16
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                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: modified_base LOCATION: (136)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                LOCATION: (158)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                               NAME/KEY: modified_base
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341 TTGACCTACTATATAAATAAGGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCA 400
                                                                    '6 aagcttcgcgagatccggatggcactcacgctggacaagaccttcacaaaatctgaaatc 65
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                                                                                                        Conservative
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Pred. No. 0.052;
0; Mismatches 48;
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                                                                                                   Score 40.6; DB 5; Pred. No. 0.28; 0; Mismatches 112;
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                Sequence 5967, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10887.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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SEQ ID NO 3015
LENGTH: 1611
TYPE: DNA
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Best Local Similarity 52.4%;
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TITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC ACIDS AND POLYPEPTIDES, TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 2976-4031
CURRENT APPLICATION NUMBER: US/10/179,131
CURRENT FILING DATE: 2002-06-21
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SHIMER JR., GEORGE H.
KESSLER, MARCO
NOLLING, JORK
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Pred. No. 0.66;
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RESULT 14
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US-09-216-393B-340
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; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5967
; LENGTH: 610
TYPE: DNA
; ORGANISM: Human
US-10-027-632-5967
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NAME/KEY: CDS
LOCATION: (1)..(867)
THER INFORMATION:
US-09-216-393B-340
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GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
TITLE REFERENCE: TX-1-C2
CURRENT PELLOATION NUMBER: US/09/216,393B
CURRENT PILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOCTWARE: Patentin version 3.1
SEQ ID NO 340
LENGTH: 867
TYPE: NAS
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 56.9
Matches 91; Conservative
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Best Local Similarity 55.1%;
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Toxoplasma
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; LOCATION: (238)..(1104)
; OTHER INFORMATION:
US-09-216-393B-343
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; TYPE: DNA
; ORGANISM: Toxoplasma gondii
US-09-216-393B-342
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GENERAL INFORMATION:
APPLICANT: Mithausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES
FILE REFERENCE: TX-1-C2
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SOFTWARE: Patentin version 3.1
SEQ ID NO 343
LENGTH: 1397
TYPE: DNA
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 342
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CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR FILING DATE: 1997-12-19
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TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES T
FILE REFERENCE: TX-1-C2
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Toxoplasma gondii FEATURE:
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AL071370 Drosophil
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AL105275 Drosophil
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AL065923 Drosophil
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ALIGNMENTS

ACCESSION VERSION KEYWORDS RESULT 1
BM398655/c
LOCUS
DEFINITION REFERENCE AUTHORS BASE COUNT ORIGIN FEATURES COMMENT SOURCE TITLE JOURNAL ORGANISM source Tetrahymena thermophila. Tetrahymena thermophila Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena. BM398655 277 bp mRNA linear EST 17 5009-0-48-D02.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence. 920 E. 58th Street, Chicago, IL 60637, USA Tel: 773 702 4374 Fax: 773 702 3172 Unpublished (2002) Contact: Turkewitz AP 1 (bases 1 to 277)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E.,
J. and Klobutcher, L. EST. Molecular Genetics and Cell Biology University of Chicago ,J. and Klobutcher,L. EST from Tetralymena thermophila, strain CU428.1, growing cells BM398655 BM398655.1 GI:18198708 Email: apturkew@midway.uchicago.edu Seq primer: T3. 51 /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SR+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
proc. Natl. Acad. Sci USA; 98: 8709-8713."
69 c 99 g 58 t /organism="Tetrahymena thermophila" /strain="CU428.1" /db_xref="taxon:5911" 1. .277 Location/Qualifiers Score 59.4; DB 10; Pred. No. 0.00025; 277 bp Length 277; Kirk, K.E., Frankel EST 17-JAN-2002

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                     found at http://bacpac.med.buffalo.edu/drosophila_bac.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fruit fly.
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                                                                                         Conservative
                                                                                                                                                                                                                                                       /note="end :
                                                                                                                                                                                                                                                                               /clone_lib="RPCI-98"
/clone="BACR26H16"
                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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GTCATGACGGATGCGGTGCTGGCCATCGAGGACACCCGCTTCTTCGAGCACGGTGGCGTG 159
                                 GATTTGGTTAAGGCAATCGTTTCTATCGAAGACCATCGCTTCTTCGACCACAGGGGGGATT 145
                                                                         CTGCTGGGCGAATTCGGCGAGGAGCGCCGCACCCTGACCCCCATCAACGAGATCCCCCAAG 219
                                                                                                         CTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAATGCCCAAGCTAATGATATTCCCCACA 85
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                                                                                                                                                   110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR), The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13 For Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Other_GSSs: AG-ND-121J5.TR
Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 529)
Shetty, J., Malek, J., Koo, H.,
Direct Submission of BAC-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bjloftus@tigr.org
This clone is from an A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             partial digest.
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301 838 3543
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/clone="AG-RD-1215"
/clone=11b="ND-TAM"
/note="Vector: pECBAC1; S
a 154 c 186 g 95
                                                                                                                                                                                                                                                                                                                                                              /strain-"PEST"
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Anopheles
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                                                                                                                                                                     2.7%;
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                                                                                                                                               Score 53.6; DB 12;
Pred. No. 0.0096;
0; Mismatches 94;
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genomic clone
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                      509
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                                                                                                                                                                                                                                                    329 AAGCAAGAAATCTTGACCTACTATATAAATAAGGTCTACATGTCTAATGGGAACTATGGA 388
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                                                                                                                                                                                                                                                                                                               Local Similarity
GAAGCAGCCCAAGACCGCCGAAACTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGATCAACTCTCACCCAACAGTTG 229
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                                                          GCGGCTTTGCTGGCCGGCATGGTGCAGTCGACCAGCGCGCTCAACCCCNTACACCAACCCC
                                                                                                                                                                        ATGCAGACAGCAGCTCAAAACTACTATGGTAAAGACCTCAATAATTTAAGTTTACCTCAG 448
                                                                                                                                                                                                                AAACCGGAGATCCTCACCCGCTACCTGAACCTGGTCTCGTTCGGAAACAACTCGTTCGGC 388
                                                                                               ATCCAGGACGCTGCCCGGACCTACTTCGGGGTCAACGCAATCGACTTGAACTGGCAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MCC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UI-HF-BROp-ajv-b-08-0-UI.rl NIH_MGC_52 Homo sapiens cDNA clone IMAGE:3075783 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 447) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www-bio.llnl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DHIOB (LTI)"
/note="Vector: pT7T3-Pac; Site_1: Not1; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: Not1; Site_2: Eco RI;
/Constructed from size fractionated cytoplasmic mRNA
(7.4-9.5kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
134 c 156 g 83 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NIH_MGC_52"
/tissue_type="lymph"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3075783"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="germinal center B cells"
/cell_line="MGC85"
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RESULT 6
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                                                                                                                                                                                                                                      ACCACGGCATGGACTTCACGCGCACCGTGGGGTCTGTCATCCATACGCTGGGCCGCAATT
                                                                                                                                                                                                                                                                                                                                                       ATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCATCGCTTCTTCGACC 134
691 bp
AG-ND-145F13.TR ND-TAM Anopheles
, DNA sequence.
BH384275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: bjloftusetigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M University BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
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Seq primer: M13 For
Class: BAC ends.
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The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="PEST"
/db_xref="taxon:7165"
/clone="hag-ND-136D6"
/clone_lib="ND-TAM"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
/note="Vector: 189 g 121 t
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0; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                 66 AAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCATCGCT 125
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                                                                                                                                                                                                                             GCAAGGTCAAGAGCCAGGGCGCCTCGACCATCACCATGCAGGT
                                                                                                                                                                                                                                                                  AAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTT
                                                                                                                                                                                                                                                                                                   TCTTCGAGCATGGCGGCGTGGACTACAAGGGCATGCTGCGTGCTGCGCCGAACCTGG
                                                                                                                                                                                                                                                                                                                          TCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAATCTGC
                                                                                         Drosophila melanogaster genome sur
BACR14D09 of RPCI-98 library from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University. College Station, Texas 77843-2123, USA using a HindIII
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Fax: 301 838 3543
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Other_GSSs: AG-ND-145F13.TF
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Department of Eukaryotic Genomics
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fruit fly
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/strain="PEST"
/db_xref="taxon:7165"
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/note="Vector: pECBAC1; Site_1: HindIII"
175 c 234 g 144 t
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rom Drosophila melanogaster
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Matches 38; Conserv
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                                                               Drosophila Eukaryota; Pterygota;
                                                                                                                                                                                                                                            Drosophila melanogaster genome survey sequence TET3 end BACR32C19 of RPCI-98 library from Drosophila melanogaste fly), genomic survey
                                                                                                                                                                  GSS
Genoscope
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                                                                                                                                                                                                              fly), genomic survey sequence.
ALO71370
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                            Muscomorpha;
                                                                                                                                            fruit fly.
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                        (bases 1 to
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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/note="end : TET3"
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                                                                                                                 melanogaster
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1 (bases 1 to 612)

Wing, R., Close, T. J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Y., Wing, R., Choi, D.W., Fenton, R.D., Choi, D.W., Fenton, R.D., Close, S.J., Oates, R. and Main, D.

Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library Unpublished (2001)

On Jun 26, 2000 this sequence version replaced gi:13187930.

Contact: Wing RA Clemson University Genomics Institute

Clemson University Genomics Institute

Clemson University Genomics Institute
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HVSMEH0088E19f Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH0088E19f,
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                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare
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Location/Qualifiers
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR32C19"
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Seq primer: AATTAACCCTCACTAAAGGG
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                                                                                          standard; RNA;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)
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/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
/tVCDMA0009 (5 to 45 DAP)"
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/cultivar="Morex"
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57.1%;
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Fax: 919.515.9500
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NC State Un
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Eukaryota; Metazo
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Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
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                                                                                                                                                                          EST.
Globodera
                                                                                                                                                                                                                                                                                                                                                                                                                                            warthog@unity.ncsu.edu
ology found. ; gt11_2pcn_r_F10_pcn_r_079.ab1.seq.screen.
                                                                            BM415379
OP20453 Mixed Stage
                                                                                                                                                                                                                                                      Similarity
95; Conser
           Eukaryota; Metazoa;
                     Globodera
                                                 BM415379.1
                                                           BM41537
                                                                   nematode Globodera
 Tylenchoidea;
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or the Biology
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                                                                                                                                                                                                                                                                                                                     /organism="Globodera pallida"
/clone_lib="Mixed Stage EST's
potato cyst nematode"
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                   pallida
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    Pokrzywa R.M., Warry
from Globodera pallida,

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eigh, NC 27695,
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  Heteroderidae;
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Last updated, Version
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e EST's from Globodera pallida,
pallida cDNA, mRNA sequence.
           Nematoda;
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Chromadorea; Tylenchida;
Heteroderinae; Globodera.
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Contact: Opperman, C
Center for the Biology of Nematode Parasitism NC State University; IACR-Rothamsted Campus Box 7615; Raleigh, NC 27695, USA Tel: 919.515.6699
Fax: 919.515.9500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAATCAAATACAACCCCTGATCAACAAAATCAGAATCCTCAACCAGCACAACCA 1999
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                                                                                                                                                                                                                                                  fruit fly.

Drosophila melanogaster

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse

Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 /hases 1 to 860)
                                                                    - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part
Collaboration with the European Drosophila Genome Project (EDC
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided project grant. The DNA was prepared from embryos by Ala and Genevieve Payan. It has been constructed in the vec
                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - BP 191 91006 EVRY cedex - FRANCE (E
                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN13D02 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: warthog@unity.ncsu.ed
gtll_2pcn_r_F10_pcn_r_079.ab
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fly), genomic survey AL109275
                                                                                                                                                                                                                                               Direct Submission
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/db_xref="taxon:36090"
/clone_lib="Mixed Stage EST's from
potato_cyst nematode"
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                                                                                                                                                                                             e Centre National de Sequencage (E-mail : seqref@genoscope.cns.fr
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Alain Bucheton
vector
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Best Local
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                                                                                This clone is from an A. gambiae BAC library (ND-TAM) provided by F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M University BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                  Seq primer: M13 Rev
Class: BAC ends.
                                                                                                                                                                                                                                                                                             Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                              Other_GSSs: AG-ND-149L20.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shetty, J., Malek, J., Koo, H., Direct Submission of BAC-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; A Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anopheles gambiae
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                                                                 partial digest
                                                                                                                                                                                                                                                                     Email: bjloftus@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    African malaria mosquito.
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Location/Qualifiers
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/note="end : T7"
134 c 113 g
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/plasmid="pBe010BAC11"
/plasmid="taxon:7227"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                       Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.3%;
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Pred. No. 0.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collins, F., Gardner, M. as sequences from Anopheles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Loftus, B.J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gambiae
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AUTHORS
TITLE
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CNS006U0/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 CCCTCCAAGGTGGATCAACTCTCACCCAACAGTTG 229
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                                                                                                                                                                                                                                      Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library, or filters for hybridization from the BACPAC Resource Center can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATATTCCCACAGATTTGGTTAAGĠCAATCGTTTCTATCGAAGACCATCGCTTCTTCGACC 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCCCCAGGGCGCCTCCACCATCACCCAGCAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha: Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS
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                                                                                                                                                                                                                           at http://bacpac.med.buffalo.edu/drosophila_bac.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submission
                                                                                    /organism="Drosophila
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14N21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:7165"
/clone="AG-ND-149L20"
/clone_lib="ND-TAM"
/clone_tib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
/ 219 c 202 g 124 t
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/strain="PEST"
                                                               /note="end
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survey sequence T7 end of BAC
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                                            329 others
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GSS 03-JUN-1999

segref@genoscope.cns.fr

part of a

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REFERENCE
AUTHORS
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BH381742/c
LOCUS
                                                                                                            BASE COUNT
ORIGIN
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Query Match
Best Local Similarity
Matches 116; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1811 AACTCACCTGCTCCACAACAACCCCCCATCAACTGAAAGTTCAAGCTCATCATCAGATAGT 1870
                                                                                                                                                                                                                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tligr.org
Email: bjloftus@tligr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from microes of larvae. The BAC
library was constituted at Toyae and The Strain Contents
The Strain Contents of the Strain Contents of Larvae of Larvae.
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BH381742
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                                                                                                                                                                                                                                                                                                                             library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest. Seq primer: M13 Rev Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
Other_GSSs: AG-ND-126M17.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shetty, J., Malek, J., Koo, H., Direct Submission of BAC-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          African malaria mosquito.
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                                                                                                                                   213
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 106; Mismatches
                                                                                                                          /organism="Anopheles gambiae"
/strain="PEST"
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/clone="AG-ND-126M17"
/clone_lib="MD-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
a 159 c 128 g 251 t
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                      2.3%;
Score 46.4; DB 12;
Pred. No. 0.72;
0; Mismatches 116;
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                                                                                                                                                                                                            326
                                                                                                                                                                                                                                                    251 CAAAGGGTATTCCAGAAGCTAAAAGAATGGTCTGTAGCGGTAAGCCTGGAGAAGAGGGTAT 192
  71
                                                                                                       GGAATGCAGACAGCTAGCTAAAACTACTATGGTAAAGACCTCAATAATTTAAGTTTACCT 445
                                       CAGTTAGCCTTGCTGGCTGGAATGCCTCAGGCACCAAACCAATATGACCCCT 497
GAAGCTGCAATGTTTGTGGCAATGCTGGAAGCTCCGAATGCAAACAACCCGT
                                                                                 GGAATTGAAATGGCTTCAAGAATCTATTTCAATAAACATACGAATGAGCTAACCCTTCCT
                                                                                                                                                                     ACGAAAGAAGAAATCATAACACTGTATTTCAATAAATTCGATTTTACCTACAATGCAAAT 132
                                                                                                                                                                                                            ACCAAGCAAGAATCTTGACCTACTATATAAATAAGGTCTACATGTCTAATGGGAACTAT 385
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Search completed: August 11, 2002, 02:09:42 Job time: 25764 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/COTUS_COMB.seq:*
    /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-771-716-3
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; Patent No. 6159469
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Matches 1999; Conserv
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Sequence 12, Appl	Sequence 21, Appl	Sequence 82, Appl	Sequence 82, Appl	Sequence 82, Appl	-		Sequence 331, App	Sequence 8, Appli	Sequence 11, Appl	Sequence 46, Appl	Sequence 4, Appli	Sequence 3, Appli	Sequence 113, App	ω `	Sequence 101, App	Sequence 99, Appl	Sequence 671, App

ALIGNMENTS

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; TYPE: nucleic ac:
; STRANDEDNESS: dou
; TOPOLOGY: linear
US-08-961-083-1
                                                                                                                                                           TELEFAX: (301) 309-85: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1999 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Choi et. al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: MSI
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
COMPUTER: H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 9410 Ke
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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9410 Key West Avenue
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100.0%;
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RESULT 2
US-08-481-435-5
US-08-481-435-5
; Sequence 5, Application US/
; Patent No. 6027906
; GENERAL INFORMATION:
APPLICANT: Balganesh, T
APPLICANT: TOwn, Christ
; APPLICANT: TOwn, Christ
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Ca
; STREET: 1155 Avenue o
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US-08-481-435-5
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FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 819-8783
TELEPHONE: (212) 354-8113
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                          Query Match 99.18;
Best Local Similarity 99.48;
Matches 1988; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: PCR cloni
CLONE: pARC 0512 :
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United State ZIP: 10036-2787
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: IN 5 FILING DATE: 01-JUL-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
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 AGCGATTCAGTTAGAACAAAAAAGCAACCAAGCAAGAAATCTTGACCTACTATAAAATAA
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AGAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACCGA
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                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICATION NUMBER: US/08,
FILING DATE: 18-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 01-SEP-1994
                                                                                                            ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                    APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
NUMBER OF SEQUENCES: 58
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                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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ADDRESSEE: Klauber &
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STREET: 411 Hackens
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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                   08/116,541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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CLONE: SPRU42
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TELEFAX: 201 343-1684
TELEX: 133521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TAAAATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGCGCAA 60
                                                                                                                                                                   GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA 420
                                                                                                                                                                                                                                                                                                                 TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA 180
ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCCTGCTTACATGGA
                                 ATCTGAAATGAAAACCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC
                                                                     TTACTTTTCAACTTCGACTTCCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTT
                                                                                                                                                                                                                                                                                 TTACTTTTCAACTTCGACTTCCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTT
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                                                                                             AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT
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99.78;
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); Mismatches 3;
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600 551 480

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371

311 300 251 240 Gaps

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Indels Length

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Gaps

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RESULT 4
US-08-600-993A-3
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TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
TYPE: nucleic acid
TYPE: nucleic both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Patent No.
                                                                                                                                                                                                                                                                         APPLICANT: MASURE, H ROBERT
APPLICANT: MOMENTA J
APPLICANT: TUOMMANEN, Elaine
TITLE OF INVENTION: BACTERIAL EXPORTED PRETITLE OF INVENTION: ACELLULAR VACCINES BANDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack Avenue
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/600,993A
FILING DATE: 1-MAR-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/245,511
FILING DATE: 18-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                            NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                612
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    Application US/08600993A
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               unknown
DNA (genomic)
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BASED THEREON
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Best Local s
Matches 946
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STRAIN: R6
IMMEDIATE SOURCE:
CLONE: SPRU42
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NAME/KEY:
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                                                                                                                                              TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA 120
                               TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT 840
                                                                                                                                                                                                            ATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC
                                                                                                                                                                                                                                                                                                                                                                                                                  TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA 180
                                                                              AACTGGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATAT
                                                                                                                                                                                                                                                                                                                                                  TTACTTTTCAACTTCGACTTCCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTT
                 TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT
                                                                                                                                                                                                                                                                                                                                                                                   AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCCAAGACCGCCGAAACTTGGTCTT
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99.78;
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Pred. No. 1.
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L.9e-278;
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                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: OUELLETTE
APPLICANT: ROY, Paul
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                3498
                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
TELEFAX: (414) 277-5591
FORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                MOLECULE TYPE:
 3438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              901
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: WISCONSI
                                82
                                                                                               22
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                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/526,840
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                                                                                                                                                                                                                                                                                                                                  ENGTH:
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                                                                                     TCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAATGCCCCAAGCTAATGATATTCC 81
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ACAACGCTTAATTGACGCATTTTTAGCGACGGAAGACAGTCGTTTTTACGATCATCACGG 3379
                               CACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCATCGCTTCTTCGACCACAGGGG 141
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                                                                                                                                                                                                                                                                                                                 : 9100 base pairs
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                                                                                                                                  Conservative
                                                                                                                                                                                                                                   Haemophilus influenzae
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1 EAST WISCONSIN AVENUE
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PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT
IDENTIFY COMMON BACTERTAL PATHOGENS AND ASSOCIATED
ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08743637B
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                                                                                                                              Score 117.2; DB 2;
Pred. No. 2e-25;
D; Mismatches 333;
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US-08-526-840B-27/c
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GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                   PRIOR APPLICATION DATA:
                                                                                          SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: QUARLES & BRADY
                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ROY, Pau
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2847 GGTGCGTCGTTTTGGCGAAGAAATGCTTACACC
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                                                                                                                                                                                                                                                                                    STREET: 411 East
CITY: Milwaukee
                   APPLICATION NUMBER:
                                                         CLASSIFICATION:
                                                                           FILING DATE:
                                                                                                                                                                                                                                                 COUNTRY:
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o. 6001564
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                                                                                                                                                                                                                                                                    Wisconsin
                                                                                                                                                                                                                                                                                                        411 East Wisconsin Avenue
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                                                                                                                                                                                                                                                     USA
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                                                                           11-SEP-1995
12-SEP-1994
                                                                                                                                                                                                                                                                                                                                                             SPECIFIC AND UNIVERSAL PROBES AND
AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE
FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
177
                                                                                                                                  Release #1.0, Version
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Best Local
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INFORMATION FOR SEQ ID NO:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: BAKER, Jean C.
2847 GGTGCGTCGTTTTGGCGAAGAAATGCTTACACC 2814
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REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85
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                                                                        TCACGGCGCAAAATTTGAATTTCGAGCCGATTATGTCACTGAAATGGTGCGTCAAGAAAT 2848
                                                                                                         ACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGATAATTACCTCAAGGAAGT 678
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NO: 27:
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Best Local S
Matches 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (212) 354-81: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                       STRAIN: DH5 al
IMMEDIATE SOURCE:
LIBRARY: PCR C
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 2487 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: SE 9
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 5
FILING DATE: 01-JUL-1994
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                          FEATURE:
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123 GCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAAGCTTTCTTGCGCAATC 182
                                                140 TTACGTTGGATCAAATCCCACCGGAGATGGTGAAAGCCTTTATCGCGACAGAAGACAGCC 199
                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
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                                                                                                                                                                      Local Similarity nes 290; Conserv
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                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
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                                                                            CCCAAGCTAATGATATTCCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCATC 122
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application Patent No. 5922540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                INFORMATION FOR SEQ ID NO:
                                                              REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
                                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Monofunctional Glycosyltransferase TITLE OF INVENTION: Gene of Staphylococcus Aureus
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APPLICANT: Jaskunas, S.Rich
APPLICANT: Skatrud, Paul L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                              Patent No. 5922540 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                             APPLICANT: Hoskins, John APPLICANT: Jaskunas, S.Ric
                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                    SOFTWARE: PatentIn Rel
                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         TITLE OF INVENTION: Monofunctional Glycosyltransferase TITLE OF INVENTION: Gene of Staphylococcus Aureus
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HYPOTHETICAL: NO
ATTORNEY/AGENT INFORMATION:
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                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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           FILING DATE:
CLASSIFICATION:
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                                                                                                                                            ZIP:
                                                                                                                                                      COUNTRY:
                                                                                                                                                                                    STREET: Lilly Corp
CITY: Indianapolis
                                           APPLICATION NUMBER:
                                                                                                                                                                        STATE:
                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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Similarity 49.9%;
91; Conservative
                                                                                                                                            46285
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                                                                                                                                                                                               E: Eli Lilly and Company
Lilly Corporate Center
                                                                                                                                                        U.S.
                                                                                                                                                                                                                                                                                      Skatrud, Paul L.
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Pred. No. 3.4e-09;
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REFERENCE/DOCKET NUMBER: X-TELECOMMUNICATION INFORMATION:

REGISTRATION NUMBER:

39,872

x-11067

Webster, Thomas D

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RESULT 10
US-09-057-720A-1
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                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09057720A Patent No. 6143868 GENERAL INFORMATION:
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Best Local Similarity 33.9%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                             APPLICANT: Peery, Robert B.
APPLICANT: Hoskins, Joann
APPLICANT: Jaskunas, S.Richard
APPLICANT: Skatrud, Paul L.
TITLE OF INVENTION: Monofunctional Glycosyltransferase
TITLE OF INVENTION: of Staphylococcus Aureus
NUMBER OF SEQUENCES: 3
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                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
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LENGTH: 807 base pairs
TYPE: nucleic acid
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                                                                                                       CITY: Indianapolis
STATE: Indiana
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                                                                                       COUNTRY:
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Pred. No. 3.4e-09;
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                                                                                                                                                          Sequence 3, Application US/09057720A Patent No. 6143868
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
 APPLICANT: Peery, Robert b.
APPLICANT: Hoskins, Joann
APPLICANT: Jaskunas, S.Richard
APPLICANT: Skatrud, Paul L.
TITLE OF INVENTION: Monofunctional Glycosyltransferase Gene
TITLE OF INVENTION: of Staphylococcus Aureus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: X-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
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LENGTH: 807 base pairs
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ANTI-SENSE:
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Eli Lilly and Company
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Pred. No. 3.4e-09;
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Lilly Corporate Center

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US-08-731-716-1
Sequence 1, Application
Patent No. 5789202
GENERAL INFORMATION:
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Best Local Similarity 33.9%;
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 807 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: x-11067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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f: U.S.
                                                                              Application US/08731716
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               Jaskunas,
                               Hoskins, JoAnn
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                S. Richard
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rosteck, Paul R. Jr.
APPLICANT: No. 5789202ris, Franklin H.
TITLE OF INVENTION: Penicillin Binding Protein From
TITLE OF INVENTION: Streptococcus Pneumoniae
NUMBER OF SEQUENCES: 3
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NAME: Webster, Thomas D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Indianapolis
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                                   TTAGAATTAAGCAAAAAATATAGTAAGGAGCAAATTCTAACCATGTACCTTAACAACGCT
                                                                   TTTTCAACTTCGACCTCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTTAGCG 304
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Pred. No. 3.4e-07;
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              TELEPHONE: 317-276-3334 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                          FILING DATE:
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosteck, Paul R. Jr.
APPLICANT: No. 5789202ris, Franklin H.
TITLE OF INVENTION: Penicillin Binding Protein From
TITLE OF INVENTION: Streptococcus Pneumoniae
NUMBER OF SEQUENCES: 3
                                               REFERENCE/DOCKET NUMBER: X-TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                              COUNTRY:
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Rockey, Pamela K.
Zhao, Genshi
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US-08-731-716-3
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Best Local Similarity
Matches 270; Conserv
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              343 GAGCUGACUGACAUCAGUAAAAAACUUGCAGAAUGCUGUUAUUGCGACAGAAGACCGUUCU 402
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                                                                                      GATATTTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCT 835
                                                                                                                                                                     CTCACAACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAAACATCTGTGG 775
                                  ACCATTGTTGATGT
                                                                                                                                                                                                             UAUUUUGAUGCGGUGGUUAAUGAAGCUGUUUCCAAGUAUAAUCUAACAGAGGAAGAGAUU
                                                                                                                                                                                                                                                TACCTCAAGGAAGTCATCAATCAAGTTG-----AAGAAGAAACAGGCTATAACCTA 715
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                                                                     AUUGUUUAUGAAAACACAUCGCUAUUUCCGAGGGCAGAGGAUGGAACGUUUGCUCAAUCA 1104
                                                                                                                                         GUCAAUAAUGGCUACCGCAUUUACACAGAGCUGGACCAAAACUACCAAGCAAAUAUGCAG
                                                                                                                                                                                                                                                                                 AUGACUUCGCAAUUGCACGAUAAGUAUGAAGGAAAAAUCUCAGAUUACCGUUACCCCUCU 924
                                                                                                                                                                                                                                                                                                                                                       AAUAUGGUUGCAGCAGGAUAUAUUGAUAAAAACCCAAGAAACCGAAGCUGCUGAAGUUGAU 864
                                                                                                                                                                                                                                                                                                                                                                                      GAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATACACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTTATCT 544
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GENERAL INFORMATION:
APPLICANT: STRAUSS, ANDREAS
APPLICANT: THUMM, GUNTHER
APPLICANT: THUMM, GUNTHER
APPLICANT: POHLNER, JOHANNES
APPLICANT: GOTZ, FRIEDRICH
TITLE OF INVENTION: METHOD FOR IDENTIFYING A
FILE REFERENCE: 10496/P65266US0
CURRENT APPLICATION NUMBER: US/09/508,542
CURRENT FILING DATE: 2000-05-16
PRIOR APPLICATION NUMBER: PCT/EP98/06136
PRIOR APPLICATION NUMBER: 97 116 841.4
PRIOR FILING DATE: 1997-09-27
PRIOR FILING DATE: 1997-09-27
PRIOR FILING DATE: 1997-09-27
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US-09-508-542-17
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (Various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as US-09-060-756-206
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APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Gordon, Stephen
APPLICANT: Billault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEO ID NOS: 743
SOFTWARE: Patentin Ver. 2.0
LENGTH: 428
TWODE: NUM
                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/09508542 Patent No. 6339174
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Patent No. 6183957
GENERAL INFORMATION:
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Best Local Similarity 50.8%;
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Search completed: June 13, Job time: 4168 sec

2002,

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; LENGTH: 1474
; TYPE: DNA
; ORGANISM: Staphylococcus carnosus
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1):.(1474)
; OTHER INFORMATION: "n" represents a, t, c, g, unknown or other
US-09-508-542-17
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NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ver
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.7%; Score 53.8; DB 4; Best Local Similarity 50.4%; Pred. No. 1.7e-06; Matches 183; Conservative 0; Mismatches 174;
                                         1642
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                                                                                                           TGATGAACTATTTGCTGGCTATACGCGTAAATATTCAATGGCTGTATGGACAGGCTATTC 1641
                                                                                                                                                                                                                                                                                                                                                                       TGCCATGAAGGAAACGACAGCCTATATGATGACGACATGATGAAA---ACAGTCTTGAC 1461
                                         TAA 1644
                                                                             agcagtgtggattaacggctttacacctcaatacactatgtcagtgtggatgggcttcag 1122
                                                                                                                                                                    tggtacttac---ggtgctgaaacttattcacaatataatttacctgataatgcagcgaa 1062
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score

Query Match Length DB

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Sequence 710, App Sequence 44, Appl Sequence 14, Appl Sequence 108, App	Sequence 217, App Sequence 2013, Ap Sequence 2013, Ap Sequence 2013, Appl Sequence 91, Appl Sequence 495, App Sequence 495, App	139, 5631, 6631 6631 1534	9325; 9325; 9325; 596; 596; 139, Pp	Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 81, Appl Sequence 145, App Sequence 1312, Ap

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US-09-536-784-1
; Sequence 1, Application US/09536784
; GENERAL INFORMATION:
GENERAL INFORMATION: et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                            TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQUENCE 
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1999 base pa
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APPLICATION NUMBER: US/09/536,784

FILING DATE: 30-0Ct-1997

CLASSIFICATION: <UDKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083

FILING DATE: OCT-30-1997

ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks

REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB340P3
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TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
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                            TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA
                                                      STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
MMDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
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STREET: 9410 Key West
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Sequence 1, Application US/09765271

GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pn
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Science
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inc
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Best Local Similarity
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TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1999 base pairs
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FILING DATE: <Unknown>
APPLICATION NUMBER: 08/961,083

FILING DATE: OCT-30-1997

ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971

REFERENCE/DOCKET NUMBER: PB340P3
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ATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC
                         ATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC
                                                                   AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT
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STRANDEDNESS: double
TOPOLOGY: linear
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Pred. No. 0;
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US-09-765-272-1
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GENERAL INFORMATION:
GENERAPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 452
Query Match
Best Local Similarity
Matches 1999; Conserv
                                                                                                                                                 TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1999 base pairs
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
                                                                                       SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION
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STREET: 9410 Key West A:
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                    NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373
                                                                                                          TOPOLOGY: linear
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Score 1999;
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                                                 ACCGATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTAT
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RESU US-6; Se; G;	ОУ	д 2	Qy Db	Qy Db	Фр	Оy	Оу	dq Qy	ОУ	ДУ	д У	Ф	Db Db	Оy	Фу
LT 0-029 0-029 quenc ENERA APPL TITL NUMB CORR AD ST	1981 1981	1921 1921	1861 1861	1801 1801	1741 1741	1681 1681	1621 1621	1561 1561	1501 1501	1441 1441	1381 1381	1321 1321	1261 1261	1201 1201	1141 1141
4 -960-81/c -960-81/c -960-81/c -960-81/c L INFORMATION: L INFORMATION: Streptococcus pneumoniae Polynucleotides and Sequences E OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences ER OF SEQUENCES: 1649 ESPONDENCE ADDRESS: DRESSE: Human Genome Sciences, Inc. REET: 9410 Key West Avenue TY: Rockville	TCCTCAACCAGCACAACCA 1999 TCCTCAACCAGCACAACCA 1999	TACCAATCCTAACAATAATACGCAACAATCAAATACAACCCCTGATCAACAAAATCAGAA 1980 	ATCAGATAGTTCAACTTCACAGTCTAGGTCAACCACTCCAAGCACAAATAATAGTACGAC 1920 	TTCTACGTGGAACTCACCTGCTCCACAACAACCACCCCATCAACTGAAAGTTCAAGCTCATC 1860 	TTGGAATATACCAGAGGGGCTCTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTCG 1800 	CGCTGCCAAAGTTTACCGCTCTATGATGACCTACCTGTCTGAAGGAAG	GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT 1680 	GACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATACGCGTAAATATTCAAT 1620 	TCAGGCTGGTAAAACAGGAACCTCTAACTATACAGACGAAGGAAATTGAAAACCACATCAA 1560 	CATGATGAAAACAGTCTTGACTTATGGAACTGGACGAAATGCCTATCTTGCTTG	AGAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACGA 1440 	TGGAACTTACTATAAACCAATGTATATCCATAAAGTCGTCTTTAGTGATGGGAGTGAAAA 1380 	CAAAAATATGGAGCAAGTAGTGAAAAGATGGCTGCTTACGCTGCCTTTGCAAATGG 1320 	AATCGACTACCCAAGTATTCACTACTCAAATGCCATTTCAAGTAACACAACCGAATCAGA 1260 	CGTGGAAACTCTAAACAAGGTCGGACTCAACCGGGCCAAGACTTTCCTAAATGGTCTAGG 1200

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Best Local Similarity 100.0%;
Matches 1999; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION: NUMBER: US/60/029,960
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                               9763
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340PP
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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           ATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC
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Pred. No. 0;
0; Mismatches
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                                                      GACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATACGCGTAAATATTCAAT
                                                                                       CATGATGAAAACAGTCTTGACTTATGGAACTGGACGAAATGCCTATCTTGCCTTGGCTCCC
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                                            GACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATACGCGTAAATATTCAAT
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RESULT 5
US-08-961-527-145/c
; Sequence 145, Application US/08961527
; GENERAL INFORMATION:
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                         Matches 1999;
                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                 STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb st
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                       TELEFAX: (301) 309-85
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LENGTH: 10711 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 391
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TITLE OF INVENTION: Strep
                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                    NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 424
                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
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RESULT 6
US-09-583-110-1312
Sequence 1312, Application US/09583110
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino
TITLE OF INVENTION: Pneumoniae for Diagnost
FILE REFERENCE: PATHO0-07A
CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
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                             Lynn Doucette-Stamm et al.

VENTION: Nucleic Acid and Amino Acid

VENTION: Pneumoniae for Diagnostics a
                              and Therapeutics
                                       Relating
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                                      Streptococcus
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PRIOR FILLING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILLING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILLING DATE: 1997-07-02
NUMBER OF SEQ ID NOS: 5322
SEQ ID NO 1312
LENGTH: 2160
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; TYPE: DNA
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US-09-583-110-1312
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           ATCAGATAGTTCAACTTCACAGTCTAGCTCCAACCACTCCAAGCACAAATAATAGTACGAC
                                                           TTCTACGTGGAACTCACCTGCTCCACAACAACCCCCCATCAACTGAAAGTTCAAGCTCATC
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                                              ttctacgtggaactcacctgctccacaacaacccccatcaactgaaagttcaagctcatc
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131

FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553

FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/107,433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
SEQUENCES REL
                                                                                                                                                                                                                ANTI-SENSE: NO ORIGINAL SOURCE
                                                                                                                                                                                                                                                          TOPOLOGY: circular MOLECULE TYPE: DNA (geno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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ADDRESSEE: GENOME THERAPEUTICS
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HYPOTHETICAL:
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                            TAAAATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAA
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LOCATION:
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ZIP: 0235
                                                                                                                                                                                                                                                                                      TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: < SOFTWARE: <Unknown>
                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (781)893-8277
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/09107433
                                                                                                                                            DESCRIPTION:
                                                                                                                                                                                                                   SOURCE:
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                                                     Score 1987.8;
Pred. No. 0;
0; Mismatches
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                                                       GGGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAACAATCGCGAAACGTCCCAGC
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                 ATCAGATAGTTCAACTTCACAGTCTAGCTCAACCACTCCAAGCACAAATAATAGTACGAC
                                                       TTCTACGTGGAACTCACCTGCTCCACAACCACCCCATCAACTGAAAGTTCAAGCTCATC
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Sequence 9325, Application PC/TUS0203987
GENERAL INFORMATION:
APPLICANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA, 028VPC
CURRENT APPLICATION NUMBER: PCT/US02/03987
CURRENT FILING DATE: 2002-02-02
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9325 the Target of Ø Compound which

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; LENGTH: 2160
; TYPB: DNA
; ORGANISM: Streptococcus p
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2160)
PCT-US02-03987-9325
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                                                                                                AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAAACATCTGTGGGATAT
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         tgttgatgtttctaacggtaaagtcattgcccagctaggagcacgccatcagtcaagtaa
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1980	ACCAATCCTAACAATAATACGCAACAATCAAATACAACCCCTGATCAACAAAATCAGA	1921	Qy
2078	acagtctagctcaaccactccaagcacaaataatagtacga	2019	Db
1920	TCAGATAGTTCAACTTCACAGTCTAGCTCAACCACTCCAAGCACAAATAATAGTAC	1861	Qy
2018	ttctacgtggagctcacctgctccacaacaacccccatcaactgaaagttcaagctcatc		Db
1860	TCTACGTGGAACTCACCTGCTCCACAACAACCCCCATCAACTGAAAGTTCAAGCTCAT	œ	Qy
1958	ttggaatataccagagggctctacagaaatggagaattcgtatttaaaaatggtgctcg	1899	Db
1800	GGAATATACCAGAGGGGCTCTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTC	1741	Qy
1898	ogctgccaaagtttaccgctctatgatgacctacctgtctgaaggaag	1839	Db
1740	CTGCCAAAGTTTACCGCTCTATGATGACCTACCTGTCTGAAGGAAG	1681	Qy
1838	ggctgtatggacaggctattctaaccgtctgacaccacttgtaggcaatggccttacggt	1779	Db
1680	CTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGG		Qy
1778	ctctcaatttgtagcacctgatgaactatttgctggctatacgcgtaaatattc	1719	Db
1620	CCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGC	1561	Qy
1718	caggctggtaaaacaggaacctctaactatacagacgaggaaattgaaaaccacatca	1659	Db
1560	GCTGGTAAAACAGGAACCTCTAACTATACAGACGAGGA	ப்	Qy
1658	gatgaaaacagtcttgagttatggaactggacgaaatgcctatcttgcttg	1599	Db
1500	ATGATGAAAACAGTCTTGACTTATGGAACTGGACGAAATGCCTATCTTGCTTG	4	Qy
1598	tatatgatgaccg	1539	Db
1440	GAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACC	1381	Qy
1538	tggaacttactataaaccaatgtatatccataaagtcgtctttagtgatgggagtgaaaa	1479	Db
	GGAACTTACTATAAACCAATGTATATATCCATAAAGTCGTCTTTAGTGATGGGAGTGAA	w	Qy
1478	. caaaaaatatggagcaagtagtgaaaagatggctgcttacgctgcctttgcaaatgg	1419	Db
	AAAAAATATGGAGCAAGTAGTGAAAAAGATGGCTGCTTACGCTGCCTTTGCAAATG	N	Qy
1418	aaccgaatcag	1359	Db
1260	TCGACTACCCAAGTATTCACTACTCAAATGCCATTTCAAGTAACACAACCGAATCA	N	Qy
1358	taaatgg	1299	Дb
1200	GTGGAAACTCTAAACAAGGTCGGACTCAACCGCGCCAAGACTTTCCTAAATGGTCTAG	\vdash	Оу
1298	cag	1239	Дb
1140	GGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAACAATCGCGAAACGTCCC		Оу
1238	cgttcacgatgagccctataactaccctgggacaaatacccctgtttataactgggatag	1179	Db
1080	GTTCACGATGAGCCCTATAACTACCCTGGGACAATACTCCTGTTTATAACTGGGATA	0	Qy
1178	accgatcacagactatgctcctgccttggagtacggtgtctacgagtcaactgccactat	1119	DЬ
1020	CCGATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTA	961	Qy
1118	tgtttccttcggaattaaccaagcagtagaaacaaaccgcgactggggatcaactatgaa		Db
960	GTTTCCTTCGGAATTAACCAAGCAGTAGAAACAAACCGCGACTGGGGATCAACTATG	901	Qy

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TITLE OF INVENTION: Identification of Es:
TITLE OF INVENTION: DONARD
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,24
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PRIOR PRIOR DATE: 2001-02-16
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US-09-815-242-9325
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APPLICANT: Ohlsen, Kathad, Ju
APPLICANT: Zyskind, Ju
APPLICANT: Wall, Danie
APPLICANT: Trawick, Jo
APPLICANT: Carr, Granth
APPLICANT: Yamamoto, F
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Best Local Similarity
Matches 1988; Conserv
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LOCATION: (1)...(2160)
-09-815-242-9325
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ORGANISM: Streptococcus
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INFORMATION:
                                                          TTACTTTTCAACTTCGACTTCCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTT
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APPLICANT: Bussey, Howard
TITLE OF INVENTION: Methods for Identifying th
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028A
CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEO ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9325
LENGTH: 2160
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APPLICANT: Xu, H
APPLICANT: Foulke
APPLICANT: zamuddi
APPLICANT: dasell
APPLICANT: Ohlset
APPLICANT: Trawic
APPLICANT: Yamann
APPLICANT: Yamann
APPLICANT: Roemes
APPLICANT: Boone
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 TYPE: DNA ORGANISM:
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Ohlsen, Kari L.
Zyskind, Judith W.
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Boone, Charles
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Yamamoto, Robert T
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Zamudio, Carlos
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                                            TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT
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US-60-061-998-596
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US-60-061-998-596/c
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TELEPAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 594
SEQUENCE CHARACTERISTICS:
LENGTH: 10333 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/6
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LAGACE, ROBERT E.
APPLICANT: CORLEY, NEIL C.
APPLICANT: RUSSO, FRANK D.
APPLICANT: HANN, AMY L.
APPLICANT: HEATH, JOE D.
APPLICANT: FINNEY, GREGORY L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Word Perfect 6.1 for Windows/MS-DOS
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REFERENCE/DOCKET NUMBER: PM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE TITLE OF INVENTION: GENOME, FRAGMENTS THEREOF, AND USES THEREOF NUMBER OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lind
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TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA 180
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ADDRESSEE: INCYTE PHARMACEUTICALS,
STRRET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Win
CURRENT APPLICATION NUMBER: US/60/068,175
FILING DATE: HEREWITH
CURSSIFICATION:
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APPLICANT:
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APPLICANT:
                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
                                                                                                                                                      APPLICANT: Heath, Joe D.
APPLICANT: Finney, Gregory L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF
TITLE OF INVENTION: GENOME, FRAGMENTS THEREO
NUMBER OF SEQUENCES: 1175
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Corley, Neil C.
Russo, Frank D.
Hann, Amy L.
                      US/60/068,175
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; CLONE: SPI
US-60-068-175-596
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REFERENCE/DOCKET NUMBER: PM-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-416
INFORMATION FOR SEO ID NO: 596:
SEQUENCE CHARACTERISTICS:
LENGTH: 9845 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: genomic DNA
INMEDIATE SONGE:
SENZC598
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                                 GTTCTACGTGGAACTCACCTGCTCCACAACAACCCCCCATCAACTGAAAGTTCAAGCTCAT
                                                                ATTGGAATATACCAGAGGGGCTCTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTC
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RESULT 13
US-08-116-541-3
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; GENERAL INFORMATION:
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                                                                                         ; LOCATION:
US-08-116-541-3
                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25
SOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,541
FILING DATE: 1933901
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 600-1-069
TELEPONMENTION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
                          Matches
                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Klauber & J
STREET: 411 Hackensack
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy di
COMPUTER: IBM PC Compa
                                                                                                                                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                 CLONE: SPR
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Masure, H. Robert
APPLICANT: Pearce, Barbara J.
APPLICANT: Toumanen, Elaine
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                                                                                                                                                                                            ORIGINAL SOURCE:
                                                                                                                                                                                                         MOLECULE TYPE: DI
HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                         LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                     STRAIN:
                                                                                                                                                                                                                                             TOPOLOGY: unknown
                                                                                                                                                                                 ORGANISM:
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APPLICANT:
APPLICANT:
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Hodgson, John
Knowles, David
Lonetto, Michael
Nicholas, Richard
                                                    Black, Michael
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611 600 551

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PCT-US97-14436-139
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1174 CGCCAAGACTITCCTAAATGGTCTAGGAATCGACTACCCAAGTATTCACTACTCAAATGC
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/02
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Stodola, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                              1294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
                1533 CAGACGAGGAAATTGAAAACCACATCAAGACCTCTCAATTTGTAGCACCTGATGAACTAT 1592
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REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US97/14436 FILING DATE: 15-AUG-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGCCAAGACTTCCCTAAATGGTCTAGGAATCGACTACCCAAGTATTCACTACTCAAATGC
                                                                                                                                       ACG-AAATGCCTATCTTGCCTTGGCTCCCTCAGGCTGGTAAAACAGGAACCTCTAACTATA 1532
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                                                                     ACGAAAATGCCTATCTTGCTTGGCTCCCTCAGGCTGGTAAAACAGGAACCTCTAACTATA
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Pred. No. 5.1e-218;
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RESULT 15
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                                                                                                                                          FILING DATE: 15-AUG-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/024,022
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Lonetto, Michael
APPLICANT: Lionetto, Michael
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: NOVEL PROKARYOTIC POLYNUCLEOTIDES,
TITLE OF INVENTION: POLYPEPTIDES AND THEIR USES
SEQUENCE CHARACTERISTICS:
LENGTH: 2172 base pair
                                                                                          REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,503
                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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CITY: King
STATE: PA
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SOFTWARE: FastSE
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Best Local Similarity 99.4%;
Matches 822; Conservative
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Search completed: June 13, Job time: 7603 sec

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Result
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Maximum DB
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Listing first 45 summaries
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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1999
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
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/cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
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US-08-961-083-1
US-09-540-2098-3719
US-09-573-476-206
US-09-673-476-626
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US-09-673-476-626
US-09-673-476-628
US-09-673-476-628
US-09-673-476-671
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US-09-540-2098-4136
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US-10-142-426-438	US-10-146-731-438	US-10-142-885-438	US-10-140-805-438	US-10-140-472-438	US-10-141-759-438	US-10-141-756-438	US-10-140-923-438	US-10-140-864-438	US-10-141-761-438	US-10-137-871-438	US-10-123-155-438	US-10-027-632-219980	US-10-105-299-11424	US-60-360-039-26589	US-60-360-039-32748	US-10-027-632-235624	US-10-104-047-1358	US-09-769-744A-121
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence												
438,	438,	438,	438,	438,			438,	438,	438,	438,	438,	219980	11424	26589	32748,	235624	1358,	121,
App	80,	4 , A	9, A	8, A	24,	, Ap	App											

ALIGNMENTS

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RESULT 1
US-08-961-083-1
                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO: US-08-961-083-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08961083 GENERAL INFORMATION:
Query Match
Best Local Similarity
Matches 1999; Conserv
                                                                                                                                                                                              TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1999 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/961,083
ETLING DATE: 30-OCC-1997
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome ScientsTreET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Choi et. al.
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae
NITMERE OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: PB340P2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland COUNTRY: USA
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                                                                                                                                                                                                                                                                             TELEPHONE: (301)
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                  100.0%;
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                    Score 1999;
Pred. No. 0;
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                                     Length 1999;
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GGGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAACAATCGCGAAACGTCCCAGC
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                                                                                               TGTTTCCTTCGGAATTAACCAAGCAGTAGAAACAAACCGCGACTGGGGATCAACTATGAA
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RESULT 2
US-10-121-120-27/c
US-10-121-120-27/c
; Sequence 27, Application U
; GENERAL INFORMATION:
; APPLICANT: Bergeron, Mich

US/10121120

a

APPLICANT: Bergeron, Michel G
APPLICANT: Ouellette, Marc
APPLICANT: Roy, Paul H.
TITLE OF INVENTION: Specific
TITLE OF INVENTION: Primers
TITLE OF INVENTION: C Rapid
TITLE OF INVENTION: Pathogen

Specific and Universal Primers

Probes

and

Amplification

to Rapidly Pathogens a

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Lect and Identify Antibiotic Resist

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                      ATCAGATAGTTCAACTTCACAGTCTAGCTCAACCACTCCAAGCACAAATAATAGTACGAC
                                                                     TTCTACGTGGAACTCACCTGCTCCACAACAACCCCCATCAACTGAAAGTTCAAGCTCATC
                                                                                                                  TCAGGCTGGTAAAACAGGAACCTCTAACTATACAGACGAGGAAATTGAAAACCACATCAA 1560
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RESULT 3
US-09-540-209B-3719
; Sequence 3719, Application
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; LENGTH: 9100
; TYPE: DNA
; ORGANISM: Haemophilus influenzae
US-10-121-120-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 5.9%;
Best Local Similarity 50.3%;
Matches 349; Conservative
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CURRENT APPLICATION NUMBER: US/10/121,120

CURRENT FILING DATE: 2002-04-11

PRIOR APPLICATION NUMBER: 09/452,599

PRIOR FILING DATE: 1999-12-01

PRIOR PRIOR DATE: 1999-12-01

PRIOR APPLICATION NUMBER: 08/304,732

PRIOR PRIOR FILING DATE: 1994-09-12

PRIOR FILING DATE: 1994-09-12

PRIOR FILING DATE: 1994-09-12

PRIOR FILING DATE: 1994-09-12

PRIOR FILING DATE: 1994-09-12
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Pred. No. 1.5e-22;
0; Mismatches 333;
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US-09-540-209B-3719
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APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 3719
LENGTH: 2370
TYPE: DNA
                                                                                                                                                                   Sequence 206, Application US/09673476 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.0%;
Best Local Similarity 46.9%;
APPLICANT: BUCHRIESER-BROSCH, ROLAND
APPLICANT: GORDON, STEPHEN
APPLICANT: BILLAULT, ALAIN
TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF
TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A
TITLE OF INVENTION: MYCOBACTERIA, APPLICATION TO THE DETECTION
TITLE OF INVENTION: MYCOBACTERIA.
FILE REFERENCE: 05394.0011-00000
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Pred. No. 2
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2.2e-06;
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CURRENT APPLICATION NUMBER: US/09/673,476
CURRENT FILING DATE: 2002-03-29

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                                                                     : LENGTH: 363
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-673-476-626
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Matches
                                                                                                                                  SOFTWARE: PatentIn Ver. 2.2
SEQ ID NO 626
LENGTH: 363
Query Match
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LENGTH: 428
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                                                                                                                                                                                         TIPLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASE TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF TITLE OF INVENTION: MYCOBACTERIA. FILE REPERENCE: 05394.0011-00000 CURRENT APPLICATION NUMBER: US/99/673,476 CURRENT APPLICATION NUMBER: US/99/673,476 CURRENT FILING DATE: 2002-03-29 PRIOR APPLICATION NUMBER: PCT/IB99/00740 PRIOR FILING DATE: 1999-04-16 PRIOR FILING DATE: 1999-04-16 PRIOR FILING DATE: 1998-04-16 PRIOR FILING DATE: 1998-04-16 PRIOR FILING DATE: 1998-04-16 PRIOR FILING DATE: 1998-04-16
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PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: Patentin Ver. 2.2
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OTHER INFORMATION: a, t,
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ORGANISM: Mycobacterium tuberculosis
FEATURE:
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Pred. No. 1.5e-05;
0; Mismatches 128
            Score 51.8;
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            Length 363;
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; OTHER INFORMATION: a, t,
US-09-673-476-438
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LENGTH: 223
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                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                   Query Match
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TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
TITLE OF INVENTION: MYCOBACTERIA.
FILE REFERENCE: 05394, 0011-00000
CURRENT APPLICATION NUMBER: US/09/673,476
CURRENT FILING DATE: 2002-03-29
CURRENT FILING DATE: 2002-03-29
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PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
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NAME/KEY: modified_base

TOTATION: (203)
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                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified_base LOCATION: (158)
OTHER INFORMATION: a, t,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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OTHER INFORMATION: a, t,
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NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mycobacterium tuberculosis
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  401 GCTCAAAACTACTATGGTAAAGACCTCAATAATTTAAGTTTACCTCAGTTAGCCTTGCTG 460
                                                                               341 TTGACCTACTATATAAATAAGGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCA 400
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                                                                                                                                                                   206 cccgacggcgctggcccggcggaacgtggtcct 240
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                                        66 ctgacccgatacttgaacctggtctcgttcggcaataactcgttcggcgtgcaggacgcg 125
                                                                                                                                                                                                                               Y Match 2.0%;
Local Similarity 48.6%;
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0; Mismatches 102;
                                                                                                                                                                                                                             Score 40.6; DB 5; Length 223; Pred. No. 0.16;
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US-10-027-632-40693/c; Sequence 40693, Application US/10027632
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US-10-027-632-5967/c
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Sequence 40693, Application US/10027632

GENERAL INFORMATION:
APPLICANT: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 10827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483
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Best Local S
Matches 76
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SEQ ID NO 5967
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
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PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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Local Similarity 55.1%;
nes 76; Conservation
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US-09-789-189-1228
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Best Local Similarity
Matches 74; Conserv
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TYPE: DNA
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Sequence 1228, Application US/09789189
GENERAL INFORMATION:
APPLICANT: Lelias, Jean-Michel
TITLE OF INVENTION: Human Polynucleotides and FILLE REPERENCE: 25436/1720
CURRENT APPLICATION NUMBER: US/09/789,189
CURRENT ETILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/183452
PRIOR FILLING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 2005
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                       ; FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)..(242)

OTHER INFORMATION: "n" at position

US-09-789-189-1228
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; LCCATION: (1)...(430)
; OTHER INFORMATION: n = A,T,C
US-10-027-632-40693
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Best Local Similarity 60.8%;
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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                                                                                                                 308 CAGTTAGAACAAAAAGCAACCAAGCAAGAAATCTTGACCTACTATAAAATAAGGTCTAC 367
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                                                                             62; Conservative
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Pred. No. 1.1;
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT FILLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 46474
LENGTH: 1611
TYPE: DNA
ORGANISM: Schizosaccharomyces pombe
US-60-360-039-46474
TYPE: DNA; ORGANISM: Human US-10-027-632-213202
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-02-24
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                                                                                                             SOFTWARE: FastSEQ
SEQ ID NO 213202
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Best Local
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                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/156,358 PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome
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                                                                                                                                                               NUMBER OF SEQ ID NOS:
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Local Similarity 53.4%;
nes 78; Conservative
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; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-60-350-039-46149
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US-09-673-476-671/c
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 46149
                                                                                                                                                 Sequence 671, Application US/09673476 GENERAL INFORMATION:
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Best Local
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Best Local Similarity
APPLICANT: COLE, STEWART
APPLICANT: BUCHRIESER-BROSCH, ROLAND
APPLICANT: BUCHRIESER-BROSCH, ROLAND
APPLICANT: BUCHRIESER-BROSCH, ROLAND
APPLICANT: GORDON, STEPHEN
APPLICANT: BILLAULT, ALAIN
TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
TITLE OF INVENTION: FORM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
TITLE OF INVENTION: DNA LIBRARY. APPLICATION TO THE DETECTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei APPLICANT: Chen, Xianf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 1.8%;
Local Similarity 52.3%;
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 Mismatches

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Pred. No. 5.2;
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Pred. No. 3.2;
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CURRENT APPLICATION NUMBER: US/09/673,476
CURRENT FILING DATE: 2002-03-29
PRIOR APPLICATION NUMBER: PCT/IB99/00740
PRIOR FILING DATE: 1999-04-16

TITLE OF INVENTION: MYCOBACTERIA. FILE REFERENCE: 05394.0011-00000

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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR TILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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                                                                                                                                                                                                                                                                                                    us-10-027-632-148124/c
                                                                                                                                                                                             Sequence 148124, Application US/10027632 GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mar
TITLE OF INVENTION: Polymorphisms in the FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
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SEQ ID NO 671
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PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
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TYPE: DNA
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OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA ; ORGANISM: Mycobacterium tuberculosis US-09-673-476-99
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Best Local Similarity 51.3
Matches 84; Conservative
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                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                Best Local
                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BILLAULT, ALAIN
TITLE OF INVENTION: A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST
TITLE OF INVENTION: FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED
TITLE OF INVENTION: DNA LIBRARY, APPLICATION TO THE DETECTION OF
TITLE OF INVENTION: MYCOBACTERIA.
FILLE REPERBUCE: 05394, 0011-00000
CURRENT APPLICATION NUMBER: US/09/673,476
CURRENT FILING DATE: 2002-03-29
CURRENT FILING DATE: 2002-03-29
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PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/060,756
PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/IB99/00740
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125 TTCTTCGACCACAGGGGGGATTGATACCATCCGTATCCTG
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                                                               261 CCCTCGGACAAGATCGCCAACACGATGAAGCTGGCGATCGTCTCGATTGAAGATAAGCGG 202
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                                                                                                   CAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCATCGC 124
                                                                                                                                           ATGGTCGACGCGAAGGGCAACACGATCGCGTGGCTGTACTCGCAGCGCCGGTTCGAGGTG 262
                                                                                                                                                                                   ATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAATGCC 64
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                                                                                                                                                                                                                                                Similarity
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Pred. No. 4.
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Search completed: June 13, 2002, 14:47:52 Job time: 7519 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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Copyright (c) 1993 - 2000 Compugen Ltd
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aphylococcus a vel human diag epidermidis c	E. coli penicillin E. coli penicillin R. eutropha Mqt pa	Mycobacterium tube H. pylori ORF 14gp H. pylori cell env	C glutamicum prote Mycobacterium tube C glutamicum prote	Propionibacterium Escherichia coli p	E. coli PBP 1B tra H. pylori inner me	E. coli PBP 1B tra Propionibacterium	PBP 1B				E. coli PBP 1A tra	E. coli penicillin	₹0	pylori ORF		S. pneumoniae peni Neisseria gonorrhe

ALIGNMENTS

RESULT AAW55063

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AAW55063 standard; Protein;

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AAW55063;

WPI; 1998-272224/24. N-PSDB; AAV27323. Choi GH, 07-MAY-1998 WO9818930-A2. Streptococcus 31-OCT-1996; 30-OCT-1997; (HUMA-) HUMAN GENOME SCI INC. Hromockyj A, pneumoniae. 96US-0029960 97WO-US19422 Johnson LS, Kunsch

detection; pneumonia; otitis media; meningitis.

Streptococcus pneumoniae; antigen; vaccine; infection; diagnosis;

Streptococcus 02-OCT-1998

pneumoniae SP001 protein.

(first entry)

protective or

Nucleic acid encoding antigenic peptide(s) from Streptococcus pneumoniae - or their epitope-containing fragments, useful in

therapeutic vaccines, and for diagnosis

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                                                       stwinspapgqppstessssssssssssstsqsssttpstnnstttnpnnntqqsnttpdqqnqn
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Pred. No. 1.1e-234;
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Matches 662
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01-JUL-1994;
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SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
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3; Mismatches 1;
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26-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
                                          WPI; 2001-611495/70
N-PSDB; AAS55689.
  New polynucleotides for
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2000US-207727P.
2000US-242578P.
2000US-253625P.
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Matches 662
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Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the printed specification, but format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
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STWNSPAPQQPPSTESSSSSSDSSTSQSSSTTPSTNNSTTTNPNNNTQQSNTTPDQQNQN
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                                                                                                               mmktvlsygtgrnaylawlpqagktgtsnytdeeienhiktsqfvapdelfagytrkysm
                                                                                                                                MMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSM
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                                                                                                                                                                 used for simultaneously diagnosing pneumococcal meningitis and identifying any antibiotic-resistant S. pneumoniae strains in a sample. The methods can be used for detecting S. pneumoniae strains resistant to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin. The assays can be adapted to detect other pathogens causing meningitis. The assays can be used to detect an antibiotic resistant strain of S. pneumoniae with a minimum inhibitory concentration (MIC) of 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and a 224 bp product. The present sequence represents a Streptococcus pneumoniae pbpla transpeptidase encoding region (TER) isolate protein
                                                                                                                                                                                                                                                                                                               A polymerase chain reaction (PCR) assays have been developed for detecting an antibiotic resistant strain of Streptococcus pneumoniae using primers based on the penicillin binding protein 2B (pbp2B) gene and the pbp1A gene. The products and methods can be used for detecting 5. pneumoniae, particularly antibiotic-resistant strains. They can be
                                                                                                                             Sequence
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RESULT
AAU35135
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23-MAY-2000;
26-MAY-2000;
The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discover antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coll, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
                                                                                                                                                               New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
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; antibacterial; drug design.
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2001US-269308P.
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Matches 347
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                                                                                yevpnvqvlpsttssapqpessstvessstkeaesssssssesapssseappsteqpass
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AAR70153 ID AAR7

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                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel gene fragments encoding specific bacterial exported - specifically of S. pneumoniae, useful as vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-115448/15.
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18-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Exp2; export protein; pbpla; plpÅ; exp1; virulence determinant; permease like propenicillin binding protein lA; pyruvate accellular vaccine; antibody.
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94US-0245511
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                                                                                                                                                                                                      46.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tuomanen
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                                                                                                                                                                                           0;
                                                                                                                                                                                                      Score 1621;
Pred. No. 4.
                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expl; exp3;
ke protein;
                                                                                                                                                                                                      1; DB 16;
4.3e-105;
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                                                                                                                                                                                                                   Length
                                                                                                                                                                                            0;
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                                                                                                                                     Matches
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Best Local Similarity
                                                                                                                                                                                                                         AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus aggalactiae) amino acid sequences of the invention. S. aggalactiae is an encapsulated bacterium which is a major pathogen of humans causing sepsis and meningitis in neonates as well as adults. The S. agalactiae antigenic polypeptides are used to vaccinate against Group B Streptococcus infections, particularly to prevent infection in new born children arising from the maternal genital tract. An immunogenic composition is useful in the preparation of a medicament for the treatment or prophylaxis of Group B Streptococcus infection. The invention does not have the disadvantages of varied response rate associated with prior art capsid polysaccharide vaccination against Group B Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptides derived from Streptococcus agalactiae are useful to provide detection of, and vaccination against, Group B Streptococcus infections, particularly to prevent infection in neonatals
                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-2000; 2000WO-GB03437.
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                             118
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122 YMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLS
                                                      62
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                                                                             QSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINKV 121
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                                                                                                         IYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNL
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DB; AASO7063.
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tis; neonate; antigenic; vaccine; infection; genital tract;
                                                                                                                                                                                                                                                                                                                                                                                          Fig 1; 178pp; English.
                                                                                                                                                                                                      462 AA
                                                                                                                                     Conservative
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                                                                                                                                                39.1%;
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                                                                                                                                              Score 1361; DB Pred. No. 1e-86;
                                                                                                                                     Mismatches
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                                                                                                                                                              DB 22;
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                                                                                                                                                              Length 462;
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RESULT
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          The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins.
                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                            23-OCT-2000;
27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                                                                                                                                          New polynucleotides for the identification and antibiotics, comprise sequences of antisense \boldsymbol{n}_{\boldsymbol{i}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus cellular
                                                                                                                                                                                                                                                                             Yamamoto
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DB; AAS52145.
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; antibacterial; drug
                                                                                                                                                                Seq ID No 5782; 511pp; English
                                                                                                                                                                                                                                                                                                                                            2000US-191078P.
2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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                                                                                                                                                                                                                                                                           Ohlsen
Xu HH;
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; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; IMMEDIATE SOURCE:
; CLONE: parc 0592 truncated PBP 1B
US-08-481-435-11
Search completed: August 11, 2002, 04:26:16 Job time: 4032 sec
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                                                                                     536 APIALROPNGOVWS 549
                                                                                                                                                         481
                                                                                                                                                                                                                             439 FTT----FDSVAQDAAEKAAVEGIPALKKQRKLSD---
                                                                                                                                                                                                                                                                                            381 QQQQIIDQELYDMLSARPL--GVQPRGGVISPQPAFMQLVRQELQAKLGDKVKDLSGVKI 438
                                                                                                                                                                                                                                                                                                                 204 MISSPNGEORLFVPRSGFPDLLVDTLLATEDRHFYEHDGISLYSIGRAVLANLTAGRTVO 263
                                                                                                                       344 EPYNYPGTNTPVYN 357
                                                                                                                                                                                 285 NGKVIAQLGARHQSSNVSF-GINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHD 343
                                                                                                                                                                                                                                                 239 LTTGMDVYTNVDQEA-------QKHLWDIYNTDEYVAYPDDELQVASTIVDVS 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 LIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNLQS-NSLQ 67 :|: | | | :: | | | | | | | | | :: |
                                                                                                                                                    SGEVRAMVG----GSEPQFAGYNRAMQARRSIGSLAKPAT-YLTALSQPKIYRLNTWIAD 535
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Query Match
Best Local Similarity
"~+~hes 77; Conserva
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US-08-600-993A-24
                                                                       ; CLONE: PARC 0593
US-08-481-435-12
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  Matches 115;
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                TELEFAX: (212) 354-81 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
                                                                                                                               MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: IN 580/MAS/94 FILING DATE: 01-JUL-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Balganesh, Tanjore S
APPLICANT: Town, Christine
TITLE OF INVENTION: NO. 6027906el Polypeptides
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                    FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,3
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
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ZIP: 100
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                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 10 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/481,435
                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10036-2787
                                                                                                                                                                                   : 532 amino acids amino acid
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  Conservative
                                                                                                                 Escherichia coli
                                                                                                                                                           linear
                                                                                                                                                                                                                                                           (212) 819-8783
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ID NO: 12:
                10.6%;
30.7%;
                                                                                     truncated soluble PBP
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  68;
Score 370.5; DB 3;
Pred. No. 6.2e-20;
58; Mismatches 138;
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                          Length 532;
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RESULT 15
US-08-481-435-11
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Patent No. 6027906
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                                                                          TELEFAX: (212) 354-81 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                          FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Balganesh, Tanjo APPLICANT: Town, Christine
                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                TELEPHONE: (212)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 NGKVIAQLGARHQSSNVSF-GINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 QQQQIIDQELYDMLSARPL--GVQPRGGVISPQPAFMQLVRQELQAKLGDKVKDLSGVKI 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 SNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLSEM 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 MISSPNGEQRLFVPRSGFPDLLVDTLLATEDRHFYEHDGISLYSIGRAVLANLTAGRTVQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 GASTLTQQLVKNLFLS---SERSYWRKANEAYMALIMDARYSKDRILELYMNEVYLGQSG 299
                                                                                                                                                      REFERENCE/DOCKET NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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STATE: New Yor
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STRANDEDNESS
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                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPYNYPGTNTPVYN 357
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                amino acid
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                                     553 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                             (212) 819-8783
212) 354-8113
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FOPOLOGY:

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US-08-245-511-24
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; Patent No. 5928900
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FILING DATE: 18-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
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                                                                                                                                                                                            TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                   MOLECULL NO HYPOTHETICAL: NO
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT: Pearce, Ba
APPLICANT: Tuomanen,
                   ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
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                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
   ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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411 Hackensack Avenue
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Pearce, Barbara J
                                                                                                                 unknown
Streptococcus pneumoniae
                                       N-terminal
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BASED THEREON
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Query Match
Best Local Similarity
Thes 77; Conserve
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24,
                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                            TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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CLONE: SPRU42
                                                                                                                                                                                                                                              FILING DATE: 01-SEP-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
            FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                   MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                       SEQUENCE CHARACTERISTICS
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                                         ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/116,541 FILING DATE: 01-SEP-1994
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0
FILING DATE: 18-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 1-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
ORGANISM:
                                                                               TOPOLOGY:
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                                                                                                         LENGTH:
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                                                                              unknown
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Streptococcus pneumoniae
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                                                    : peptide
NO
                         N-terminal
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; Pred. No. 6.20
0; Mismatches
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RESULT 11
US-08-481-435-9
; Sequence 9, Application US/08481435
; Patent No. 6027906
; Patent No. 6027906
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Best Local
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                                                                       GENERAL INFORMATION:
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MOLECULE TYPE: p
ORIGINAL SOURCE:
APPLICANT: Balganesh, Tanjore S
APPLICANT: Town, Christine
TITLE OF INVENTION: No. 6027906el Polypeptides
NUMBER OF SEQUENCES: 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 14.7%; Score 512; DB 3; 1
Local Similarity 28.6%; Pred. No. 2.5e-30;
les 201; Conservative 99; Mismatches 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPYNYPGTNTPVY---NWDRGY--FGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNQGYISAEQYEKAVNTPITDGLQSLKSA-SNYPAYMDNYLKEVI----NQVEEETGYNL: | | | | : | : | : : | : : | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLYLSEM 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINKVYM---- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNLQS-NSLQ 67
                                                                                                                                                                                                    SEMQQ----
                                                                                                                                                                                                                                                                                                 DGS--EKEFSNVGTRAMKETTAYMMTDMMKTVLTYGTGR--NAYLAWLPQAGKTGTSNYT 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGIDYPSIHYSNAI---SSNTTESDKKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFS 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGKVIAQLGARHQSSNVSF-GINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTT----FDSVAQDAAEKAAVEGIPALKKQRKLSD---------LETAIVVVDRF 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTTGMDVYTNVDQEA------QKHLWDIYNTDEYVAYPDDELQVASTIVDVS
                                                                                                                                                                                                                                      SSTSQSSSTTPSTNNSTTTNPNNNTQQSNTTPDQQNQNPQPAQ 665
                                                                                                                                                                                                                                                                            LA-NQTPTPLNLVPPEDIADMGVDYDGNFVCSGGMRILPVWTS-----
                                                                                                                                                                                                                                                                                                                                                                                  DEEIENHIKTSQFVAPDELFAGYTRKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMWTY 571
                                                                                                                                                                                                                                                                                                                                                                                                                        DGKVLYQSFPQ-AERAVPAQAAYLTLWTMQQVVQRGTGRQLGAKYPNLHLAGKTGTTN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGVPKDQLHPVPAMLLGALNLTPIE------VAQAFQTIASGGNRAPLSALRSVIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APIALRQPNGQVWSPQNDDRRYSESGRVMLVDALTRSMNVPTVNLGMALGLPAVTETWIK 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SGEVRAMVG----GSEPQFAGYNRAMQARRSIGSLAKPAT-YLTALSQPKIYRLNTWIAD 535
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                                                                                                                                                                                                  ---- QPSGNPFDQSSQPQQQPQQ-QPAQ 824
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Matches
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CLONE: PARC046
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ORIGINAL SOURCE:
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LENGTH: 836 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 819-8783
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                     204 MISSPNGEQRLFVPRSGFPDLLVDTLLATEDRHFYEHDGISLYSIGRAVLANLTAGR--- 260
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OPERATING SYSTEM:
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nes 197; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/481,435
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                                                                                           GKVIAQLGARHQSSNVSF-GINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDE 344
                                                                                                                                                                                                         QQQIIDQELYDMLSARPL--GVQPRGGVISPQPAFMQLVRQELQAKLGDKVKDLSGVKIF 431
                                                                                                                                                                                                                                                                               NEIRGEPLASLYYEGRPVEELSLDQQALLVGMVKGASIYNPWRNPKLALERRNLVLRLLQ 373
                                                                                                                                                                                                                                                                                                                                                                                              GSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINKVYM----S 124
                                                        GEVRAMVG----GSEPQFAGYNRAMQARRSIGSLAKPAT-YLTALSQPKIYRLNTWIADA 528
                                                                                                                                  TT----FDSVAQDAAEKAAVEGIPALKKQRKLSD---
                                                                                                                                                                     TTGMDVYTNVDQEA------QKHLWDIYNTDEYVAYPDDELQVASTIVDVSN 285
                                                                                                                                                                                                                                                                                                     NGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLSEMK 184
                                                                                                                                                                                                                                          NQGYISAEQYEKAVNTPITDGLQSLKSA-SNYPAYMDNYLKEVI----NQVEEETGYNLL 239
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.0%; Score 489; DB 3; Length 836; 28.1%; Pred. No. 1.3e-28; tive 97; Mismatches 274; Indels 134;
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US-08-481-435-7
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US-08-481-435-7
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 354-811
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01-JUL-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION DATA:
PRIOR APPLICATION UNBER: IN 580/MAS/94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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ADDRESSEE: White & Case
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   239 LTTGMDVYTNVDQEA----
                                  381
                                                              184 KNQGYISAEQYEKAVNTPITDGLQSLKSA-SNYPAYMDNYLKEVI----NQVEEETGYNL 238
                                                                                                 321
                                                                                                                                124
                                                                                                                                                              264
                                                                                                                                                                                                                          204 MISSPNGEQRLFVPRSGFPDLLVDTLLATEDRHFYEHDGISLYSIGRAVLANLTAGRTVQ 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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                               QQQQIIDQELYDMLSARPL--GVQPRGGVISPQPAFMQLVRQELQAKLGDKVKDLSGVKI
                                                                                                                             SNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLSEM 183
                                                                                                                                                            GASTLTAALVKNLFLS---SERSYWRKANEAYMALIMDARYSKDRILELYMNEVYLGQSG
                                                                                                                                                                               GGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINKVYM---- 123
                                                                                                                                                                                                                                                  LIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNLQS-NSLQ 67
                                                                                              DNEIRGFPLASLYYFGRPVEELSLDQQALLVGMVKGASIYNPWRNPKLALERRNLVLRLL
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6027906 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8,
TELEFAX: (212) 354-81: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                APPLICATION NUMBER: IN 580/MAS/94 FILING DATE: 01-JUL-1994 PRIOR APPLICATION DATA:
                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 819-8783
                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TOWN, CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                    TELEPHONE:
                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                  NAME: Sterner, Richard J
REGISTRATION NUMBER: 35,
                                                                                                                                                              FILING DATE:
                                                                                                                                                                              APPLICATION NUMBER:
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55 Avenue of the
                                                                                                                                                              24-NOV-1994
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                  354-8113
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                            STATE: New York
COUNTRY: United States
ZIP: 10036-2787
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,435
FILING DATE: 10-JUL-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08481435 Patent No. 6027906
                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 'CORRESPONDENCE ADDRESS'
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Balganesh, Tanjore S
APPLICANT: Town, Christine
               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                     CITY: New York
STATE: New Yor
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QALRQVGSNIKPFL-YTAAMDKGL--TLASMLND------VPISRWDASAGSDWQPK 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPTYGPLLPAAVTSANPQQATAMLADGSTVALSMEGVRWARPYRSDTQQGPTPRKVTDVL 402
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                                                                                                                                                                                                                                                                          1155 Avenue of the
                                                                                                                                                                                                                                                                                             White & Case
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                                                                                                                                                                                                                                                                                                                              No. 6027906el Polypeptides 42
IN 580/MAS/94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---GTRAMKETTAYM-MTDMMKTVLTYGTGRNAY-----
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                                                                                                                                                                                                                                                                          Americas
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Best Local 9
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TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 823 amino acids
TYPE: amino acid
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FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 1103326-151 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 01-JUL-1994 PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 35,
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SEMQQ--
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                                                                                                                                                                                                                                            DGKVLYQSFPQ-AERAVPAQAAYLTLWTMQQVVQRGTGRQLGAKYPNLHLAGKTGTTN--
                                                                                                                                                                                                                                                                                   DGS--EKEFSNVGTRAMKETTAYMMTDMMKTVLTYGTGR--NAYLAWLPQAGKTGTSNYT 511
                                                                                                                                                                                                                                                                                                                                                                                                                                   EPYNYPGTNTPVY---NWDRGY--FGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTTGMDVYTNVDQEA-----QKHLWDIYNTDEYVAYPDDELQVASTIVDVS
                                    SSTSQSSSTTPSTNNSTTTNPNNNTQQSNTTPDQQNQNPQPAQ 665
                                                                               LA-NQTPTPLNLVPPEDIADMGVDYDGNFVCSGGMRILPVWTS----
                                                                                                                    LSEGSNPEDWNI--PE----GLYRNGEFVFKNGAR--STWNSPAPQQPPSTESSSSSSD 622
                                                                                                                                                          ----NNV-----DTWFAGIDGSTVTITWVGRDNN-QPTKLYGASGAMSIYQ---RY
                                                                                                                                                                                                                                                                                                                              LGVPKDQLHPVPAMLLGALNLTPIE-----VAQAFQTIASGGNRAPLSALRSVIAE 625
                                                                                                                                                                                                                                                                                                                                                                    LGIDYPSIHYSNAI----SSNTTESDKKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFS
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Best Local
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 828 amino acids
TYPE: amino acids
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                             NNSTTTNPNNNTQQ---SNTTPDQQ
                                                                                                                                                       VAPDELFAGYTRKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIP
                                                                                                                                                                                       TPLAFLIKSALNTNIFGEPGWQGTGWRAGRDLQRRDIGGKTGTTN------
                                                                                                                                                                                                                       TESDKKYGASS---EKMAAAYAAFANGGTYYKPMYIHKVVFSDG--------
                                                                                                                                                                                                                                                                                                                                                                              NSPPQYAGPIRLRQGLGQSKNVVMVRAMRAMGVDYAAEYLQRFGFPAQNIVHTESLA---
                                                                                                                                                                                                                                                                                                                                                                                                                                              QALRQVGSNIKPFL-YTAAMDKGL--TLASMLND------VPISRWDASAGSDWQPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETNRDWGSTMKPITDYAPALEYGYYDSTATIVHDEPYNYPGTNTPVYNWDRG-----
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----LANGGNSREEYFIEGTQPTQQ 809
                                                                                          EGLYRNGEFVFKNGARSTWNS-----PAPQQP--PSTESSSSSSSSSTSQSSSTTPST
                                                                                                                         SSKDAWFSGYGPGVVTSVWIGFDDHRRNL ---GHTTASGAIKDQISGYEGGA-----
                                                                                                                                                                                                                                                    IPVIYGDTQKSNVLENNDVEDVAISREQQNVSVPMPQLEQANQALVAKTGAQEYAPHVIN
                                                                                                                                                                                                                                                                                  ----SEKEFSNV------GTRAMKETTAYM-MTDMMKTVLTYGTGRNAY-----
                                                                                                                                                                                                                                                                                                                 -----LGSASFTPMQVARGYAVMANGGFLVDPWFISKIENDQGGVIFEAKPKVACPECD
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                                                            --KSAQPAWDAYMKAVLEGVPEQPLTPPPGIVTVNIDRSTGQ------
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                            Matches 200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: IN 580/MA.
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 940407
FILING DATE: 24-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 354-81 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Balganesn, range APPLICANT: Town, Christine TITLE OF INVENTION: NO. 60
                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NO. NUMBER OF SEQUENCES: 42 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
226
                                180 LSEMKNOGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINOVEE---ETGY 236
                                                                                                                                              109
                                                                                                                                                                                                                      49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                      1 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRIL-GAFLR 59
                                                                                       KVYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLV 179
                                                                                                                                                             NLQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYIN 119
                                                                                                                                                                                                                      QIYSADGELIAQYGEKRRIPVTLDQIPPEMVKAFIATEDSRFYEHHGVDPVGIFRAASVA 108
LSRMLDEGYITQQQFDQTRTEAINANYHAPETAFSAPYLSEMVRQEMYNRYGESAYEDGY
                                                                        KIYLGYRAYGVGAAAQVYFGKTVDQLTLNEMAVIAGLPKAPSTFNPLYSMDRAVARRNVV
                                                                                                                                              LFSGHASQGASTITAALARNFFLS---PERTLMRKIKEVFLAIRIEQLLTKDEILELYLN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'RY: United States 10036-2787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     850 amino acids
                                                                                                                                                                                                                                                                                          Conservative 129; Mismatches 246; Indels 290;
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10-JUL-1995
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24-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354-8113
                                                                                                                                                                                                                                                                                                          15.9%; Score 555; DB 3; 23.1%; Pred. No. 1.4e-33;
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TOPOLOGY: linear; MOLECULE TYPE: protein US-08-731-716-2
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; Sequence 2, A
                                                                                                                                                                                                                                                                             Matches 192;
                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGLESTRALLON NUMBER: X-REFERENCE/DOCKET NUMBER: X-TELECOMMUNICATION INFORMATION: 317-276-3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Penicillin Binding Prote: TITLE OF INVENTION: Streptococcus Pneumoniae NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 731 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Webster, Thomas D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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182 EMKNQGYISAEQYEKAVNTPIT----DGLQSLKSASNYPAYMDNYLKEVI---NQVEEET 234
                                                                       122 YMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLS 181
                                                                                                               152 TAGRSGGGSTITQQLAKNAYLS---QDQTVERKAKEFFLALELSKKYSKEQILTMYLNNA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
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                                                                                                                                 62 QSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINKV 121
                                                                                                                                                                                                 95
                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
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                                                                                                                                                                                                                                  2 IYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNL 61
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                                     YFGNGVWGVEDASKKYFGVSASEVSLDQAATLAGMLKGPELYNPLNSVEDSTNRRDTVLQ
                                                                                                                                                                                             IFDREEKEAGALSGQKGTYVELTDISKNLQNAVIATEDRSFYKNDGINYGRF---FLAIV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN 304
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                                                                                                                                                                                                                                                                                               Similarity
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Lilly Corporate Center
                                                                                                                                                                                                                                                                           Conservative 108;
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VENTION: Penicillin Binding Protein From
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhao, Genshi
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Rockey, Pamela K.
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27.7%;
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, S. Richard
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                                                                                                                                                                                                                                                                         Score 636; DB 1;
Pred. No. 8.2e-40;
8; Mismatches 252
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                                                                                                                                                                                                                                                                           252;
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                                                                                                                                                                                                                                                                                                            Length 731;
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                                                                                                                                                                                                                                                                         Gaps
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US-08-481-435-2
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                                                                                                                                                                    APPLICATION NUMBER: US/08/481,435
FILLING DATE: 10-UUL-1995
CLASSIFICATION: 45
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IN 580/MAS/94
FILING DATE: 01-UUL-1994
                  REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                            FILING DATE: 24-NOV-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
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                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
TELEPHONE:
                                                                                                                                   APPLICATION NUMBER: SE 9404072-2
                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: United States ZIP: 10036-2787
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                                                                            Sterner, Richard
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US-08-245-511-4
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Best Local Similarity
Matches 315; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILLING DATE: 01-SEP-194
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Masure, H Robert
APPLICANT: Pearce, Barbara J
APPLICANT: Tuomanen, Elaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
 301
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                                                                                                                                                     181
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                                                                                                                                                                                                             121 VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
TYPE: amino acid
TOPOLOGY: lines-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                                                                        61 LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/01 FILING DATE: 18-MAY-1994
                                                                                                                                                                                                                                                                                                                                                 S
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 VSFGINQAVETNRDWG 316
                                                             TGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN 300
                                                                                                                                    SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT 240
                                                                                                                                                                                                                                                                                                                                               KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 64
                                                                                                                                                                                         VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 184
                                                                                                                SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT 244
                                                                                                                                                                                                                                                                    LQSNSLQGGSALTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 124
                                       TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN

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99.7%;
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Pred. No. 6.7e-115;
0; Mismatches 1;
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Patent No.
                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
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INFORMATION FOR SEQ ID NO:
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APPLICANT:
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TOPOLOGY: linear
MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-194
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 18-MAY-1994
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
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181 SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT 240
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                                                                         121 VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
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Local Similarity 99.7%;
les 315; Conservative
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                                                      VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 184
                                                                                                                               LQSNSLQGGSALTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 124
                                                                                                                                                LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
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Pearce, Barbara J
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Pred. No. 6.7e-115;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                    Length 320;
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                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08481435 Patent No. 6027906
                                            STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 1035-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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APPLICANT:
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            APPLICATION NUMBER: US/08/481,435 FILING DATE: 10-JUL-1995 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                 PQPAQP
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APPLICATION DATA:
                                                                                                                                                                                 E: White & Case
1155 Avenue of
                                                                                                                                                                                                                                                  Town, Christine
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Best Local Similarity
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TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 819-8783
TELEFAX: (212) 354-8113
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: IN 5:
FILING DATE: 01-7UL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9.
FILING DATE: 24-NOV-1994
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LENGTH: 682 amino acids
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Maximum Match 100%
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1: /ggn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-481-435-1
US-08-481-435-2
US-08-481-435-9
US-08-481-435-9
US-08-481-435-12
US-08-481-435-12
US-08-71-716-12
US-08-71-716-12
US-08-71-716-12
US-08-71-716-12
US-08-75-720A-2
US-08-481-435-13
US-08-75-720A-2
US-08-289-75-1
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US-09-206-800-1
US-09-206-808-1
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US-09-206-898-3	US-09-206-800-3	US-08-589-756-3	US-09-206-898-23	US-09-421-868-2	US-08-293-728-2	US-08-456-670B-40	US-08-525-742-8	US-08-483-101-4	US-08-551-459-4	US-09-136-605-7	US-09-003-687A-7	US-08-821-355A-7	US-08-450-582-7	US-08-450-582-2	US-08-452-655B-7	US-08-452-655B-2	US-08-452-654-7
Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 23, Appl	2,	Sequence 2, Appli	Sequence 40, Appl	Sequence 8, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 7, Appli

ALIGNMENTS

; MOLECULE TYPE: protein US-08-961-083-2 RESULT 1 US-08-961-083-2 ; Sequence 2, Application US/08961083 ; Patent No. 6159469 GENERAL INFORMATION: APPLICANT: Choi e REFERENCE/DOCKET NUMBER: PB TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504 TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 2: COMPUTER: HP Vectra 486. OPERATING SYSTEM: MSDOS SOFTWARE: ASCII Text CURRENT APPLICATION DATA: APPLICATION NUMBER: US/ ATTORNEY/AGENT INFORMATION: NAME: Brookes, A. Anders CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: COMPUTER READABLE FORM: MEDIUM TYPE: Diskett SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS: TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: $452\,$ LENGTH: 666 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear ZIP: NAME: Brookes, A. Anders REGISTRATION NUMBER: 36, FILING DATE: FILING DATE: CITY: Rockville STATE: Maryland COUNTRY: ADDRESSEE: 20850 E: Human Genome Sciences, Inc. 9410 Key West Avenue HP Vectra 486/33 Diskette, MSDOS version 6.2 US/08/961,083 36,373 3.50 inch, PB340P2 1.4Mb

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1 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 60

Matches

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; DB 4; 2.3e-255; es 0;

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Gaps

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Length Indels

Query Match Best Local Similarity THIS PAGE BLANK (USPTO)

Db 603 ysyfmrnilaiepslkrkfdvpkglrk--eivdkipyysspnsitp-tpkktdds 654

Search completed: August 11, 2002, 04:25:30 $\,$ Job time: 4356 sec

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29-MAR-1996;
02-APR-1996;
25-OCT-1996;
28-OCT-1996;
Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent infection and for diagnosis of H. pylori infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis.
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Claim 14; Pages 780-781; 1145pp; English.

This sequence is a H. pylori protein of unspecified function.

The protein may be used in a vaccine to prevent or treat H. pylori compounds, infection or to identify H. pylori polypeptide binding compounds, cuseful as potential H. pylori life cycle activators or inhibitors. The CDNA and probes derived from it may be used for the identification of card sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies against the protein can be used in immunoassays to evaluate the abundance and itstribution of H. pylori-specific antigens. The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions can development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR camplification for recombinant polypeptide production, e.g. in E. coli

Sequence 660

δÃ ρy DЬ Š В Qy 밁 Qy 멍 Ωy Q Qy 밁 Q B γQ В Qy Вþ 밁 Query Match Best Local S Matches 185 449 448 337 238 179 165 119 565 500 391 342 282 277 108 60 48 7.9%; Score 625; DB 18; Local Similarity 28.2%; Pred. No. 4.3e-35; Pres 185; Conservative 129; Mismatches 255 1 KIYDNKNQLIADL-GSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLR 59 naksgryteggstltgqlvknmvl---trektltrklkeaiisiriekvlskeeileryl 164 YRSMMTYL--SEGSNPEDWNIPEGLYRNGEFVFKNGARSTWNSPAPQQPPSTESS NLQSNS-LQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYI 118 pdtarnfengn---ysknsvqnhawhpsnytrkflglvtlqealshslnlatinlsdqlg HDEPYNYPGTINTPVY------NWDRGYFGNITLQYALQQSRNVPAVETLNKVG DVSNGKVIAQLGARHQSSNVSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIV 341 LLTTGMDVYTNVDQEAQKHLWDIY----VLSEMKNQGYISAEQYEKAVN-TPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYN 237 sn-----nni-----dawfigftptlqsviwfgrddn-tp-igkgatggvvsapv SNYTDEEIENHIKTSQFVAPDELFAGYTRKYSMAVWTGYSNRLTPLVGNGLT---VAAKV fekiyqslsdmgfknlpkdlsivlgs-----faispidaaekyslfsnygtmlkpml LNRAKTFLNGLGIDYPSIHYSNAISSNTTESDKKYGASSEKMAAAYAAFANGGTYYKPMY lktqgytikltidldyqrlaleslrfghqkilekiakekpktnasndkdednlnasmivt 336 ilrrlyslgwissnelksalnevpivynqtstqniapy-----vvdevlkqldqldg--NKVYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNL 178 iesitnqqnevktftpietkkitskeqafltlsalmdavengtgslarikgleiagktgt IHKVVFSDGSEKEFSNVGTRAM-KETTAYMMTDMMKTVLTYGTGRNAYLAWLPQAGKTGT -----NTDEYVAYPDDELQVASTIV 255; Length 660; Indels 86; Gaps 448 499 447 507 281 559 276 22;

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48 60 Query Match Best Local S Matches 185

Local Similarity 28.2 nes 185; Conservative

17.9%; Score 625; DB 18; 28.2%; Pred. No. 4.3e-35; tive 129; Mismatches 255;

Length 660; Indels 8

Gaps

22;

KIYDNKNQLIADL-GSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLR :| | | ::::::| | | |: :: | ::

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108 119

164 178

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This sequence is a H. pylori cell envelope inner membrane protein convolved in outer membrane and cell wall synthesis. The protein may be converted in a vaccine to prevent or treat H. pylori infection or to identify converted the pylori polypeptide binding compounds, useful as potential H. pylori converted the pylori converted from it converted to the cycle activators or inhibitors. The DNA and probes derived from it converted to the pylori infection. Nucleic acid sequences complementary converted to the DNA act as antisense sequences and can be used to prevent the converted to the DNA act as antisense sequences and can be used to prevent the converted to the pylori sequence of H. pylori can be used in immunoassays to evaluate the abundance and distribution of converted the pylori specific antigens. The genomic sequence of H. pylori can be used in immunoassays to evaluate the abundance and distribution of convertance in the protein can be used in immunoassays to evaluate the abundance and distribution of converted the pylori specific antigens. The genomic sequence of H. pylori can be used for off of the pylori antigens for converted by computer evaluation. To identify likely H. pylori antigens for converted development, the amino acid sequences predicted from various ORF converted pylori can be used for significant homology to other known or exported converted interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-DEC-1996;
29-MAR-1996;
02-APR-1996;
25-OCT-1996;
28-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. infection and for diagnosis of H. pylori infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claims 14,80; Page 747-749; 1145pp; English.
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trans-peptidation activity;

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant Streptococcus pneumoniae useful in screening assays for antiba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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Zhao G;
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                                                                                                    -NYPGTNT----PVYNWDRGYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGI
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                                                                                                                                                                GARHQSSNVSF-GINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPY----
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                                                                                                                                                                                                                                                                      EMKNQGYISAEQYEKAVNTPIT----DGLQSLKSASNYPAYMDNYLKEVI----NQVEEET
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Pred. No. 8.5e-36;
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02-SEP-1998;
02-SEP-1998;
                                             AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54575 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodizes and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (a.g. meningities and contributions).
                                                                                                                                                                                                                                                                                    Fraser C,
Petersen
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antibacterial; gene t
Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may all be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the inventi
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                                                                  AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54576 and AAZ54576 and AAZ5476 to AAZ54737 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Meisserial bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention
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H, Venter JC;
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Sequence

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Penicillin-binding protein; PBP-Nv; transglycolase; antibacterial agent;

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ismatches 261;
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02-SEP-1998;
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    Petersen
                       Fraser C,
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                                                                                                                                      NITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESDKKYG
                                                                                                                                                                                                           THRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTN-----TPVYNWDRGYFG
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)B; AAZ54365.
                                                  ASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKE-----
                                                                                                     yitlrqaltasknmvsirilmsigvgyaqqyirrfgfrsselpaslsmalgtget----
                                                                                                                                                                        amrqpgstfkpfv-ysaalskgm--tastvvndapislpgkgpngsvwtp-knsdgrysg
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                                -tplkvaeaysvfanggyrvsshvidkiydrdgrlraqmqplvagqnapqaidprnayim
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Best Local
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              14-FEB-2002
                                         AAU37184;
                                                                     AAU37184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLOSN-SLOGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYI 118
                                                                                                                                         tnrsthggsdtsanssgtagsnnntrsggsrn
                                                                                                                                                                     TPST---NNSTTTNPNNNTQQSNTTPDQQNQN
                                                                                                                                                                                                                          SNP----EDWNIPEGLYRNGEFVFKNGARSTWNSPAPQQPPSTESSSSSSSSSTSQSSST
                                                                                                                                                                                                                                                                                   TSQFVAPDEL - - - - FAGYTRKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEG
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                                                                     standard;
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Pred. No. 1.8e-48;
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                                                                                                                                                                                                                                   The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential CC genes, themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used CC to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen cfor homologous nucleic acids which are required for cell proliferation in essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part
                                                                                                                                                     Query Match
Best Local Similarity
Matches 222; Conserv
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23-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                              of the printed specification, format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides for the identification and develorantibiotics, comprise sequences of antisense nucleic
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27-NOV-2000;
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16-FEB-2001;
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             119
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                                                                                                                             1 KIYDNKNQLIADL-GSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLR
NLQSN-SLQGGSTLTQOLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYI
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-253625P.
2000US-257931P.
2001US-269308P.
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Xu HH;
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32.1%; Pred. No. 1.8e-48;
tive 128; Mismatches 261
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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                                                                                                                                                            Score
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Gapop 10.0 , Gapext 0.5
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/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
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Copyright (c) 1993 - 2000 Compugen Ltd
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19
   9 US-09-536-784-2

1 US-09-765-271-2

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9 US-09-583-110-3973

5 US-09-107-433-3705

PCT-US02-03987-13423

2 US-09-815-242-13423
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1091.692 Million cell updates/sec
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Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3973, Ap
Sequence 3705, Ap
Sequence 13423, A
Sequence 13423, A
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RESULT 1 US-09-536-78 ; Sequence 2 ; GENERAL 2 ; GENERAL 1 NUM COR COR COR COR ATT		110 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
OR RE PU RECEIVE		3466 1862.5 1862.5 1751 1751 1751 1751 1751 1473.5 1473.5 1473.5 817
Choi:		11111111111111111111111111111111111111
CATION US/0953678 ITON: Choi et. al. SEQUENCES: 452 ENCE ADDRESS: SSEE: Human Genom F: 9410 Key West Rockville RATYland RY: USA RY: USA RY: USA RY: USA RY: USA ITON USABLE FORM: EADABLE FORM: EADABLE FORM: EADABLE FORM: EADABLE OSISKETTE RER: HF Vectra 18 EATON NUMBER: US ATION NUMBER: US G DATE: 30-Oct-19 IFFICATION LOTA: CATION NUMBER: 08 G DATE: 007-30-19 SENT INFORMATION MICHELES: MATK MICHELES: MIMBER: MATK MICHELES: MIMBER: MATK MICHELES: MIMBER: MATK MICHELES: MIMBER: MATK MICHELES: MATK MICHELES: MIMBER: MATK MICHELES: MIMBER: MATK MICHELES: MICHEL		719 823 823 777 823 777 89 877 7727 7727 7727 7727 7727 772
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784 tococcus pneumoniae tococcus pneumoniae me Sciences, Inc. t Avenue t Avenue 1.4Mb 486/33 DOS version 6.2 US/09/536,784 1997 nown> 08/961,083	ALIGNMENTS	US-10-072-851-13423 US-9-107-532-5667 US-99-107-532A-5667 PCT-US02-03987-10728 US-99-815-442-10728 US-98-816-541-4 US-99-814-238-26 US-09-814-238-26 US-09-814-238-26 US-09-814-238-26 US-09-815-242-5782 US-09-815-242-5782 US-09-815-242-5782 US-09-815-242-12777 US-10-072-851-12777 US-10-072-851-12777 US-10-072-851-12777 US-10-072-851-222-4572 US-09-614-529-451-2277 US-09-614-529-451-2821 US-09-614-529-451-2821 US-09-634-238-283 US-09-634-238-283 US-09-634-238-283 US-09-328-552-4373 US-09-328-552-4373 US-09-328-352-4373 US-09-328-352-6216 PCT-US97-05223-876 US-08-761-318-845 US-08-824-132-876 US-08-824-132-876 US-08-824-132-876 US-08-933-002A-5603
Antigens and Vaccines		Sequence 13423, A Sequence 5667, Ap Sequence 10728, A Sequence 239, Appl Sequence 22, Appl Sequence 5782, Ap Sequence 5782, Ap Sequence 12777, A Sequence 12777, A Sequence 12777, A Sequence 12777, A Sequence 2412, Ap Sequence 2421, Ap Sequence 2431, Ap Sequence 2431, Ap Sequence 3814, Ap Sequence 311825, A Sequence 11825, A Sequence 4707, A Sequence 4708, App Sequence 845, App Sequence 845, App Sequence 876, App

REFERENCE/DOCKET NUMBER: PB340P3

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RESULT 2
US-09-765-271-2
; Sequence 2, Application US/09765271
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Best Local S
Matches 666
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TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                               KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD 480
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TOPOLOGY: linear;

MOLECULE TYPE: protein;
SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQ
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 666 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/536,784
ETILING DATE: <UNKNOWN>
APPLICATION NUMBER: 08/961,083
ETLING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genom
STREET: 9410 Key West
                                                                                                                                                                                                                                                                                       VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
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                            VSFGINQAVETNRDWGSTMKPITDYAPALEYGYYDSTATIVHDEPYNYPGTNTPYYNWDR
                                                                                                                                                                                                                             SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD
                                                                                                                                                    TGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                                                                                                                                                                                                                                                   LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                                                                                                                                                                                                                                                                   LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                                                                                                                               SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
                                                                                                                                                                                                                                                                        VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       al Similarity
666; Conserv
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STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 41,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 22-Jan-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 3.50 inch, COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION DATA
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Pred. No. 3e-289;
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US-09-765-272-2
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Best Local S
Matches 666
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                                                                                                                                                                                                                                                             TELEFAX: (301) 309-8:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                      Local Similarity
   61
                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PB340P2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                             KIYDNKNQLIADLGSERRVNAQANDIPTDLYKAIVSIEDHREFDHRGIDTIRILGAFLRN 60
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                              KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/765,272 FILING DATE: 22-Jan-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                              LENGTH: 666 amino acids
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                                                                                    100.0%; Score 3484; DB 21.
ilarity 100.0%; Pred. No. 3e-289;
Conservative 0; Mismatches 0;
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                                           Query Match
Best Local Similarity
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; ORGANISM: Streptococcus US-09-583-110-3973
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                                                                                                                                     NUMBER OF SEQ ID NOS:
SEQ ID NO 3973
LENGTH: 719
TYPE: PRT
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                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/583,110
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/085,131
                                                                                                                                                                                                   APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococc TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics FILE REFERENCE: PATHOO-07A
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                         100.0%;
                                                                                                                   pneumoni
%; Score 3483;
%; Pred. No. '
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                                              DB 19;
                                          Length 719;
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1 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 60

Mismatches No. 4.2e-289; smatches 0;

Indels

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RESULT 5
US-09-107-433-3705
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GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,433
ETLING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                          NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            MMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSM
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                                                                                                                                                        CITY: Waltham
STATE: Massachusetts
                                                                                                                                 ZIP: 02354
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SEQUENCES REL
THERAPEUTICS
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Best Local Sim
Matches 665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMÁTION:
NAME: Axiniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
                                                                                                                                                                                                             GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD 420
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                                                         AVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGAR
                                                                                                                                                                                                                                                                                    VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR 360
                                                                                                                                                                                                                                                                                                                            LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
              STWNSPAPQQPPSTESSSSSSSSSSTSQSSSTTPSTNNSTTTNPNNNTQQSNTTPDQQNQN
                                                                                                                 MMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEELENHIKTSQFVAPDELFAGYTRKYSM
                                                                                                                                                          KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD
                                                                                                                                                                       KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD 480
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                                            AVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGAR
                                                                                                    MMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSM
 LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/ 08513
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 721 amino acids
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(781)893-8277
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1; Mismatches 0;
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; ORGANISM: Streptococcus PCT-US02-03987-13423
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PCT-US02-03987-13423
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TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA 0.28 VPC
CURRENT APPLICATION NUMBER: PCT/US02/03987
CURRENT FILING DATE: 2002-02-02
PRIOR APPLICATION UNUBER: 60/267,636
PRIOR APPLICATION UNUBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13423
LENGTH: 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13423, Application PC/TUS0203987
GENERAL INFORMATION:
APPLICANT: Elitra Pharmaceuticals, Inc.
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Best Local
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                                                                                                 MMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSM 540
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                                                                                                                                                                                                                                         GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
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STWNSPAPQQPPSTESSSSSSSSSSTSQSSSTTPSTNNSTTTNPNNNTQQSNTTPDQQNQN 660
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                                                                                                                                                                      KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD
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Pred. No. 1.2e-287;
3; Mismatches 1;
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RESULT 7
US-09-815-242-13423
US-09-815-242-13423
US-09-815-242-13423
GENERAL INFORMATION:
GENERAL INFORMATION:
Description:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PRILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 13423
LENGTH: 719
TYPE: PRT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/269,308 PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 662; Conserv
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                                                                                                                                                                                                                                                                                                             LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                                                                                                                                                                   VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
                                                                  TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                                                                         SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
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VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR 360
                                            TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                                                    SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
                                                                                                                                                                                                                           VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
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Pred. No. 1.2e-287;
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                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/072,851
CURRENT FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 18811
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13423
LENGTH: 719
                                                                                                             Query Match 99.3
Best Local Similarity 99.4
Matches 662; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13423, Application US/10072851 GENERAL INFORMATION:
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APPLICANT:
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TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Carr, Grant J. APPLICANT: Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: ELITRA.028A
                                                                                                                                                                                                                  TYPE: PRT
481
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Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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Yamamoto, Robert T.
Roemer, Terry
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Zamudio, Carlos
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                                                                                                                            99.5%;
                                                                                                                                                                                                  pneumoniae
                                                                                                            Score 3466; DB 24;
Pred. No. 1.2e-287;
3; Mismatches 1;
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Sequence 5667, Application US/09107532
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm &
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                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER:
                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICATION NUMBER: 60/0 FILING DATE: July 2, 199 ATTORNEY/AGENT INFORMATION:
                                      APPLICATION NUMBER: 60/ 01 FILING DATE: May 14, 1998 PRIOR APPLICATION DATA:
                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532
                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                  FILING DATE: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                         OPERATING SYSTEM: SOFTWARE:
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              60/051571
2, 1997
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REGISTRATION NUMBER:

Ariniello, Pamela Deneke

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; LOCATION: 1...823
US-09-107-532-5667
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Best Local Similarity
Matches 371; Conserv
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INFORMATION FOR SEQ ID NO: 5667:
SEQUENCE CHARACTERISTICS:
LENGTH: 823 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: GTO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: pro
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                   653
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 773
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                                                                                                                                                                                                                                                                                                                                                                     241 TGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN | :::|||:| :|| ||:|| ||:| : :
                                                                                                                                                                                                                                                                                                                                                                                                          295
                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                             235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QYMGTITLRQALYLSRNVPAVKLFNEVGSDKVASFLKNLGIEYSTIHQSNAISSNTEEQD
                                                                                                                                                                                                                                                                  GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD 420
                                                                                                                                                                                                                                                                                                    --TTNPNNNTQQSNT----TPDQQNQNP 661
                                                                                                                         MAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYR-NGEFVFKN-
                                                                                                                                                   DILKDTITEGTGTNAQIAGLYQAGKTGTSNYTDDEYAK-LGISSGVYPDILFAGYTPNYS
                                                                                                                                                                DMMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYS
                                                                                                                                                                                                                                                                                                                                                       YTMLQNEXISQTEYDQAVNVPVTDGLQELTQSDDNTKIVDNYVXEVINEYQEKTDXNVYT
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT 240
SSTTVPSSSSEESSTPSSSAPPASSSEP
                                                                                                ISVWTGYNKKMTPVTSESSHVASDVYRELMQYVSANVTNTDWEMPSGLIRVGGELYYKDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          VYMSNGLYGMETASEMYFGKKLSELSLPQTALLAGMPQAPSAYDPYVYPDQAKKRRDTVL
                                               YTARSNAITPSTTIPSSSYVQTPGSSTTETTTQSSSSTSQSESTAESSKESTTAETSEPA
                                                                       *GARSTWNSPAPQQP-----PSTESSSSSSDSSTSQSSSTTPSTNNST-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.5%; Score 1862.5; DB 15
53.9%; Pred. No. 7e-150;
100. Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15;
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                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...823; SEQUENCE DESCRIPTION: SEQ ID NO: 560 US-09-107-532A-5667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-09-107-532A-5667
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Best Local S
Matches 371
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GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (781)893-8277 INFORMATION FOR SEQ ID NO: 5667:
                                                                                                                                                                                                                                   115
 241
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                                                                                                                                                                                                                                                                                              Local Similarity
nes 371; Conserv
                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                  MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                               VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
                                                                                                                                                                                                                                 TGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN 300
                               YTMLQNEKISQTEYDQAVNVPVTDGLQELTQSDDNTKIVDNYVKEVINEVQEKTDKNVYT
                                                  SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT 240
                                                                                                 VYMSNGLYGMETASEMYFGKKLSELSLPQTALLAGMPQAPSAYDPYVYPDQAKKRRDTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 823 amino acids
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                                                                                                                                                                                                                                                                                                 Score 1862.5; DB
Pred. No. 7e-150;
9; Mismatches 17
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AND AMINO ACID SEQUENCES
FAECIUM FOR DIAGNOSTICS A
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                                                                                                                                                                                                                                                                                                                                  DB 15;
                                                                                                                                                                                                                                                                                                                                  Length 823;
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Sequence 10728, Application PC/TUS0203987
GENERAL INFORMATION:
APPLICANT: Elitra Pharmaceuticals, Inc.
TITLE OF INVENTION: Methods for Identifying the
TITLE OF INVENTION: Proliferation
FILE REFERENCE: ELITRA.028VPC
CURRENT APPLICATION UNMBER: PCT/US02/03987
CURRENT FILING DATE: 2002-02-02
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 15811
SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10728
LENGTH: 778
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Enterococcus
PCT-US02-03987-10728
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PCT-US02-03987-10728
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261
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                                                                                                                                                                                                                                                                                                                                                 Local Similarity 51.4 nes 347; Conservative
                    SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
                                                                                                           VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
YTMYDNKKISKAEYEKAKATPIDEGLVPLKASDDNRKVVDNYVKEVINEVKAKTGKNVYT
                                                                                                                                                                        VKNGGLQGGSTLTQQLIKLSYFSTKESDQTLKRKAQEAWMAVRLEREKSKEEILTYYINK
                                                                                                                                                                                             LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                                                                                                                                                                        KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QYMGTITLRQALYLSRNVPAVKLFNEVGSDKVASFLKNLGIEYSTIHQSNAISSNTEEQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR 360
                                                                                    VYMANGFYGMETAAENYYGKHLSELDLPQTALLAGMPQAPNSYDPYTKPDTAKERRDVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --TTNPNNNTQQSNT---TPDQQNQNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YTARSNAITPSTTIPSSSYVQTPGSSTTETTTQSSSSTSQSESTAESSKESTTAETSEPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYR-NGEFVFKN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DMMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTKYGASSLKMAAAYAAFANGGTYYKPQYVNKIVFQDGTEETYEPDGKTAMSPETAYMIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GARSTWNSPAPQQP------PSTESSSSSSDSSTSQSSSTTPSTNNST-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISVWTGYNKKMTPVTSESSHVASDVYRELMQYVSANVTNTDWEMPSGLIRVGGELYYKDQ
                                                                                                                                                                                                                                                                                                                                               50.3%; Score 1751; DB 1; 51.4%; Pred. No. 2.4e-140; rative 125; Mismatches 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     faecalis
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                                                                                                                                                                                                                                                                                                                                                                                          Length 778;
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                    ; TYPE: PRT ; ORGANISM: Enterococcus US-09-815-242-10728
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                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/815,24
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/211,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10728, Appl GENERAL INFORMATION:
                                                                                  SOFTWARE: FastSEQ
SEQ ID NO 10728
LENGTH: 778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith
                                                                                                                                                 NUMBER OF SEQ ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Identification of Essential Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: ELITRA.011A
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Trawick, John D.
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Zyskind, Judith W.
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Sequence 10728, Application US/10072851
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GENERAL INFORMATION:
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
APPLICANT: Foulkes, J. Gordon
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
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 TINVENTION:
                                                                Trawick, John D.
Yamamoto, Robert
Roemer, Terry
                                        Jiang, Bo
Boone, Charles
                                                                                                            Wall, Daniel
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Pred. No. 2.4e-140;
5; Mismatches 193;
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; FILE REFERENCE: ELITRA.028A
; CURRENT APPLICATION NUMBER: US/10/072,85
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 15811
; SOFTMARE: FASTSEQ for Windows Version 4.
; SEQ ID NO 10728
; LENGTH: 778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKNGGLQGGSTLTQQLIKLSYFSTKESDQTLKRKAQEAWMAVRLEREKSKEEILTYYINK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTTSRKAQEAWLAIQLEQKATKQEILTYYINK 120
SSAEQPATSEQPPEP
                            TTPDQQNQNPQPAQP 666
                                                                                                                                        MAVWTGYSNRLTPLVGNGLTVAAKYYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGA
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                                                                                                                                                                                  DMLKDVLNGGTGFNGAIPGLIQAAKTGTSNYTDEDLARMGTTEKGIAPDSTFVGYTTHYA
                                                                                                                                                                                                                                             GDKYGISSLKLAAAYAAFANNGIYNKPYYVNKVVFNDGTSVDYQPDGKRAMKDSTAYMMT
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                                                            YEVPNVQVLPSTTSSAPQPESSSTVESSSTKEAESSSSSSSESAPSSSEAPPSTEQPASS
                                                                                        RSTWN------SPAPQQPPSTESSSSSSSSTSQSSSTTPSTNNSTTTNPNNNTQQSN
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pred. No. 2.4e-140;
5; Mismatches 193;
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US-09-134-000-4939
Sequence 4939, Application US/09134000A
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
NOTITLE OF INVENTION: NUCLEIC ACID AND AMINO

ACID

SEQUENCES RELATING

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ENTEROCOCCUS

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; TITLE OF INVENTION: FAECALIS FOR DIAGNOSTICS AND FILE REFERENCE: GTC-005
; CURRENT APPLICATION NUMBER: US/09/134,000A
; CURRENT FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 6810
; SEQ ID NO 439
; LENGTH: 789
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000-4939
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Sequence 4, Application US/08116541
GENERAL INFORMATION:
APPLICANT: Masure, H. Robert
APPLICANT: Pearce, Barbara J.
APPLICANT: Toumanen, Elaine
TITLE OF INVENTION: BACTERIAL E
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Best I
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                                                                                                                                                           SSAEQPATSEQPPEP
                                                                                                                                                                                         TTPDQQNQNPQPAQP 666
                                                                                                                                                                                                                                                                                   VSVWTGYNDRNTPIYQEYYGIASDVYREIMSYLSQNVSNDDWYQPDSVVRVGNELYVKDA
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                                                                                                                                                                                                                        YEVPNVQVLPSTTSSAPQPESSSTVESSSTKEAESSSSSSSSAPSSSEAPPSTEQPASS
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                                                                                                                                                                                                                                                                                                                                                                   DMMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTMYDNKKISKAEYEKAKATPIDEGLYPLKASDDNRKYVDNYVKEVINEVKAKTGKNVYT
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BACTERIAL EXPORTED
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Pred. No. 2.4e-140;
25; Mismatches 193;
   PROTEINS
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; MOLECULE TYPE:
US-08-116-541-4
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Matches
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DC SOFTWARE: PatentIn Release #1. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Jackson Egg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ACELLULAR VACCINES NUMBER OF SEQUENCES: 45
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STREET: 411 Hackens
CITY: Hackensack
STATE: New Jersey
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les 315; Conserva
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                                                                                                                                                                                                                                                                                                   VSFGINQAVETNRDWG
                                                            TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                            TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN
                                                                                                                                       SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
                                                                                                                                                                                 VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
                                                                                                                                                                                              VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
                                                                                                                                                                                                                                        LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
VSFGINOAVETNRDWG
                                                                                                                        SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 7.2e-130;
0; Mismatches 1;
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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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Sequence 122, App
Sequence 8941, Ap
Sequence 9358, Ap
Sequence 6, Appli
Sequence 10183, Ap
Sequence 522, App
Sequence 408, App
Sequence 3, Appli
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11, Appli
12, Appli
130, Appli
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	5358,	10169,	6575, 1	9843, A	29528,	8783, Ap	v	8784, Ap	28206,	7548, AI	310, Ap	22243,	11155,	1608, Ap	18499,	9976, Ap	34, Appi	28204,	

ALIGNMENTS

RESULT 1 US-08-961-083-2 ; Sequence 2, Application US/08961vv. ; GENERAL INFORMATION: ; APPLICANT: Choi et. al. ; TITLE OF INVENTION: Streptococcus pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **UNMBER OF SEQUENCES: 452 **TITLE OF INVENTION: Streptococcus pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: Streptococcus pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: Streptococcus pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: Streptococcus pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: Streptococcus pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: Streptococcus pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: Streptococcus pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: Streptococcus pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: Streptococcus pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: Streptococcus pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: Streptococcus pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: Streptococcus pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: Streptococcus pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: STREPTOCOCCUS pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: STREPTOCOCCUS pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: STREPTOCOCCUS pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: STREPTOCOCCUS pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: STREPTOCOCCUS pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: STREPTOCOCCUS pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: STREPTOCOCCUS pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: STREPTOCOCCUS pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: STREPTOCOCCUS pneumoniae Antigens (NUMBER OF SEQUENCES: 452 **TITLE OF INVENTION: STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ TELEFAX: (301) 309-8: INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: PRIOR APPLICATION DATA: APPLICATION NUMBER: <Unknown> FILING DATE: <Unknown> ATTORNEY_AGENT INFORMATION: NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373 TELEPHONE: (301) 309-8504 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/961,083 FILING DATE: 30-oct-1997 CLASSIFICATION: <Unknown> COUNTRY: USA ZIP: 20850 COMPUTER READABLE FORM: OPERATING SYSTEM: MSDOS SOFTWARE: ASCII Text MEDIUM TYPE: Diskette, 3.5 COMPUTER: HP Vectra 486/33 TYPE: amino acid LENGTH: 666 amino acids STATE: Maryland 309-8512 ID 3.50 inch, 1.4Mb storage NO: version 6.2 PB340P2 and Vaccines

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1 KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 60

Query Match Best Local Similarity Matches 666;

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Score 3484; DB 4; Pred. No. 8e-225;); Mismatches 0;

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FILE REFERENCE: PWC/P21122WO
CURRENT APPLICATION NUMBER: US/09/769,744A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: PCT/GB99/02452
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: GB 9816336.3
PRIOR FILING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/125329
PRIOR APPLICATION NUMBER: US 60/125329
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 122
LENGTH: 821
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GENERAL INFORMATION:
APPLICANT: Le Page, Richard WF
APPLICANT: Wells, Jeremy M
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APPLICANT: Hanniffy, Sean B
APPLICANT: Hansbro, Philip M
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                                TYPE: PRT
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US-09-540-209B-8941

Sequence 8941, Application US/09540209B

GENERAL INFORMATION:
APPLICANT: GATY L. Breton

TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC

TITLE OF INVENTION: FOR DIAGNOSTICS AND THER

FILE REFERENCE: 2709.1001-001

CURRENT APPLICATION NUMBER: US/09/540,209B

CURRENT EILING DATE: 2000-04-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA-----AYAAFANGGTYYKPMYIHKVVFSDGS-EKEESNVGTRAMKETTAYMM 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPASTTKPLLAYGIAIDQGLMGS-ETILSNYPTNFANGNPIMYANSKG-TGMMTLGEALN 514
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NUMBER OF SEQ ID NOS: 10444 SEQ ID NO 8941 LENGTH: 789

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US-09-540-209B-9358
                                                                                                     Sequence 9358, Application US/09540209B
GENERAL INFORMATION:
APPLICANT: GATY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
CURRENT APPLICATION NUMBER: US/09/540,209B
CURRENT FILING DATE: 2000-04-04
           NUMBER OF SEQ ID NOS: 10444
SEQ ID NO 9358
LENGTH: 790
TYPE: PRT
ORGANISM: B.fragilis
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                        SMAVWTGYSNR----LTPLVGNGLTVAAKVYRSMM--TYLSE--GSNP-EDWNIPEG 586
                                                                                                                                                                                                                                                                                                                                                                                                           MLRAVINEGTGARVRRYGITADMGGKTGTTNRNS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                MMKTVLTYGTGRNA--YLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKY 538
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Sequence 6, Application US/09914543
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: LAM, David
APPLICANT: MATHUR, Eric
TITLE OF INVENTION: ENDOGLUCANASES
FILE REFERENCE: DIVER1150-5
; TYPE: PRT
; ORGANISM: Bankia
US-09-914-543-6
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Best Local S
Matches 136
                                                 NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 875
                                                                                                                  CURRENT APPLICATION NUMBER: US/09/914,543
CURRENT FILING DATE: 1998-11-22
PRIOR APPLICATION NUMBER: PCT/US97/08793
PRIOR FILING DATE: 1997-05-22
PRIOR APPLICATION NUMBER: US 08/651,572
PRIOR FILING DATE: 1996-05-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                ----YGFRDAWAVGVTPKYAVGVWVG
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Query Match Best Local Similarity

4.6%; 21.1%;

Score Pred.

162; No. 0.

DB 5;

Length

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                                                                                                                                                                        NUMBER OF SEQ ID NOS: 10194
SEQ ID NO 10183
LENGTH: 738
TYPE: PRT
                                                              Query Match
Best Local Similarity
Matches 148; Conserv
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APPLICANT: KESSLER, MARCO
APPLICANT: VOLLING, JORK
APPLICANT: ZENG, QIANDONG
APPLICANT: GREENE, JONATHAN R.
TITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC
TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/179,131
CURRENT FILING DATE: 2002-06-21
                                                                                                                                                                                                                                                                                FILE REFERENCE: 2976-4031
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HARE, ROBERTA S. APPLICANT: SHAW, KAREN J.
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               50 TIRILGAFLRNLQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKAT 109
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21.1%;
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                                                              ; Score 161; DB 6;
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92; Mismatches 290
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                                                                                               Length 738;
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RESULT / US-09-882-227-522 . Sequence 522, Application US/09882227
SOFTWARE: FastSEQ for Windows SEQ ID NO 522; LENGTH: 2893; TYPE: PRT ORGANISM: Helicobacter pylorius-09-882-227-522
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                        APPLICANT: Tomb, Jean-Francois
APPLICANT: Ocomen, Raymond P.
TITLE OF INVENTION: Encoding Novel Helicobacter Polypeptides
TITLE OF INVENTION: Genome
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/047002
                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/882,227 CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kleanthous, Harold APPLICANT: Al-Garawi, Amal
                                                                                                   NUMBER OF SEQ ID NOS: 638
SOFTWARE: FastSEQ for Windows
                                                                                                                                          PRIOR FILING DATE: 1997-07-29
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                                                                                                      Version 4.0
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GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
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APPLICANT:
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                                                   APPLICANT: Ocomen, Raymond P.
TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding Novel Helicobacter Polyn
TITLE OF INVENTION: Genome
FILE REFERENCE: 06132/047002
                 CURRENT APPLICATION NUMBER: US/09/882,227
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 08/902,615
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Local Similarity 19.5%; Pred. No. 0.12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              -----NGARSTWNSPAPQQPPSTESSSSSSSSSSSSSSTTSTTNPNNNTQQSN 651
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Tomb, Jean-Francois
                                                                                                                                                                                       Al-Garawi, Amal
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; PRIOR FILING DATE: 1997-07-29
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: FASTSEQ for Windows Version 4.
; SEQ ID NO 408
; EENCTH: 615
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-882-227-408
                                                                                                      ; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PATENTIN VET. 2.0
; SEO ID NO 3
; LENGTH: 930
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-200-650D-3
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    Query Match
Best Local Similarity
Matches 155; Conserv
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Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hook, Magnus A.O.
APPLICANT: Perkins, Samuel L.
TITLE OF INVENTION: Extracellular Matrix-Binding Proteins from Staphylococcus
FILE REFERENCE: P06283US2/BAS
                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/200,650D CURRENT FILING DATE: 1998-11-25 PRIOR APPLICATION NUMBER: 60/066,815 PRIOR FILING DATE: 1997-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Foster, Timothy APPLICANT: Eidhinn, Deird
                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/098,427 PRIOR FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 GYVQKQEEDKLT---LTTGKKGVEKS-----QDHLLKAQQNGIRTGKRDVSFNFIQNHS 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    386 KVGLN-RAKTFLNGL-----GIDYP-----SIHYSNAISSNTTESDKKYG----AS 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 YTEVERLDGYEVYLSVPLKLQREIETLLDKTK-----DKLKAKEILVGIINPKSGEILS 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEKMAAAYAAFANGGTYYKPMYIHKVVFSDG-----SEKEFSNVGTRAMKETTAYM 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------GMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSN---GKVIA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTDMMKTVLTYGTGRNAYLAWLPQAGKTGTS 508
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      Conservative
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                        4.48;
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%; pred. No. 0.018;
64; Mismatches 125; Indels 118;
; Score 153.5; DB 5;
; Pred. No. 0.074;
96; Mismatches 288;
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59 RNLQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYI 118

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RESULT 10
US-10-179-131-5286
US-10-179-131-5286
; Sequence 5286, Application US/10179131
; GENERAL INFORMATION:
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                             CURRENT APPLICATION NUMBER: US/10/179,131
CURRENT FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 10194
SEQ ID NO 5286
LENGTH: 973
                                                                                                                     APPLICANT: ZENG, QIANDONG
APPLICANT: GREENE, JONATHAN R.
TITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 2976-4031
                                                                                                                                                                                                                                               APPLICANT: HARE, ROBERTA S.
APPLICANT: SHAW, KAREN J.
APPLICANT: SHIMER JR., GEORGE
                                                                                                                                                                                                             APPLICANT:
             TYPE: PRT
ORGANISM: Candida
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                                                                                                                                                                                                             KESSLER, MARCO
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                                                                              RESULT 11
PCT-US02-19220-4
Sequence 4, Application PC/TUS0219220
GENERAL INFORMATION:
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859 PINNNHITNTTTAPTTTTTNSNPNNNNNNQDGQTMQ 894
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                                       PSTNN---STTTNPNNNTQQSNTTPDQQNQNPQPAQ
                                                                                   SSRVKQQQQQQHQHPLSRENSFSNHYDFDNRLPSPNYALGTNSSTMVSPSSDTFLLDEST
                                                                                                                           PA------SDSST--SQSSST-----T
                                                                                                                                                                   SSPLPPPSLPQSQANLHIVPEEKSRDLSHTGKDETTGTISNLLLQFNDNRSKVSDDEFNS
                                                                                                                                                                                                             SNP-----EDWN---IPEGLYRNGEFVFKNGARST---
                                                                                                                                                                                                                                                       SNSLNALLRRESLSNNNSNNSTNFQRLDSNGNIVGELNFNNNNNPKSNRSSSSEKYMTQL
                                                                                                                                                                                                                                                                                                 PDELFAGYTRKYSMAVWTGYSNRLTPLVGNGLTVA-----AKVYRSMMT--YLSEG
                                                                                                                                                                                                                                                                                                                                           DTHENTPIVKSWRANTESDSKLARISNGSLATVNTENLFSVRLIDDYSVRNSETSSKFLS
                                                                                                                                                                                                                                                                                                                                                                                   GTGRNAYL--AWLPQA------GKTGTSN-----YTDEEIENHIKTSQFVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVSSSSSSSTSSSSSTASASSSFGSSESSSSPIAHKKS----NKNKALAIGLGVGIPVF
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Similarity 19.0%; Pred. No. 0.099;
55; Conservative 91; Mismatches 312; Indels 2
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                                         665
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APPLICANT: FOSTER, Timothy
TITLE OF INVENTION: CROSS-REACTIVE MONOCLONAL
FILE REFERENCE: PO726JUS01/BAS
CURRENT APPLICATION NUMBER: PCT/US02/19220
CURRENT FILING DATE: 2002-06-17

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                Sequence 6592, Application US/09540209B
GENERAL INFORMATION:
APPLICANT: Gary L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1001-001
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LENGTH: 2283
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Best Local
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SOFTWARE: PatentIn version 3.1
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   CURRENT APPLICATION
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Local Similarity 20.6%; Pred. No. 0.57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 SNSLQGGS-----TLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYY
                                                                                                                                                                                                TSLSESASTSDSISISNSIANSQSASTSKSDSQS
                                                                                                                                                                                                                                                                    ESLSTSTSDSLRTSTSLSDSLSMSTSGSLSKSQSLSTSISGSSSTSASLSDSTSNAISTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGNIT-LQYALQQSRNVPAVETLNKVGLNRAKTF-----LNG----LGIDYPSIHYSNA 411
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NUMBER: US/09/540,209B
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NUMBER OF SEQ ID NOS: 1
SEQ ID NO 6592
LENGTH: 188
TYPE: PRT
ORGANIOM: B. fragilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/083,259
PRIOR FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34, Application US/09673605A
GENERAL INFORMATION:
APPLICANT: The President and Fellows of Harvard College
TITLE OF INVENTION: REGULATION OF BIOFILM FORMATION
FILE REFERENCE: 00246/505003
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.2%; Score 147.5; DB 5; Best Local Similarity 22.7%; Pred. No. 0.099; Mismatches 291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Escherichia
  334
                                                                                                                                                                                                                                                                                                    120 KV-----YMSNGNYGMQTAAQNYYG--KDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAA 172 : | | | ; | ; | ; | ; | ; | ; ; |
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                                                                                                                                                                                                                                                                                                                                                          5 INTNSL---SLITQNNINKNQSALSSSIERLS----SGLRINSAKDDAAGQAIANRFTS
  YDSTATIVHDEPYNYPGTNTPVYNWDRGYFGNITL---QYALQQSRNVPAVETLNKVGLN 390
                                       KDGDTVTIKADAAQTATVYTYNASAGNFSFS-NVSNNTSAKAGDVAASLLPPAGQTASGV
                                                                                                                     LNGFNVNGSGTIANKAATISDLTAAKMDAATNT-----ITTTNNALTASKALDQL
                                                                                                                                                    ETGYNLLTTG-------MDVYTNVDQEAQKHLWDIYNTDEYVAYPD--DEL 274
                                                                                                                                                                                                                                                                                NIKGLTQAARNANDGI-SVAQTTEGALSEINN-NLQRIRELT--VQASTGTNSDSDLDSI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASIIPKPKHFRNSFNNDMQLKESLEGYYRLITERLVKKGIISEVAADSIRPEIN
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                                                                            QVASTIVDVSNGKVIAQLGARHQSS-NVSFGINQAVETNRDWGSTMKPITDYAPALEYGV 333
                                                                                                                                                                                                 QDEIKSRLDEIDR----VSGQTQFNGVNVLAKDGSMKIQVGANDGQTITIDLKKIDSDTLG
                                                                                                                                                                                                                                      QDRRNLVLSEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEE
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27.6%;
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10444
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Pred. No. 0.018;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 127;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens US-09-442-489B-2
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Vogelstein, Bert
APPLICANT: White, Raymond L.
TITLE OF INVENTION: APC Antibodies
FILE REFERENCE: 001107.78817
CURRENT APPLICATION NUMBER: US/09/442,489B
CURRENT FILING DATE: 1999.11-18
PRIOR APPLICATION NUMBER: US 08/452,654
PRIOR FILING DATE: 1995-05-25
PRIOR FILING DATE: 1995-05-25
PRIOR FILING DATE: 1994-08-12
PRIOR APPLICATION NUMBER: US 08/289,548
PRIOR APPLICATION NUMBER: US 07/741,940
PRIOR FILING DATE: 1991-08-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
US-09-442-489B-2
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                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 130; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Albertsen, Hans
APPLICANT: Anand, Rakesh
APPLICANT: Carlson, Mary
APPLICANT: Groden, Joanna
APPLICANT: Hedge, Philip
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 154
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                        56
PNQYDPYSHPEAAQDRRN----LVLSEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNY 215
                                                                            KATKQEILTYYINKVYMSNGNY-----GMQTAAQNYYGKDLNNLSLPQLALLAGMPQA 159
                                                                                                                                                    AFLRNLQSNS------LQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTGTSNYTDEEIENHIKTSQFVAPDEL--FAGYTRKYSMAVWTGY-----SNRLTPL 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAKTFLNGL---GIDYPSIHYSN--AISSNTTESDKKYGASSEKMAAAYAAFANGGTYYK 445
                                      KALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYV---
                                                                                                              AVTNLNNTTTNLSEAQSRIQDADYATEVSNMS---KAQIIQQAGNSVLAKANQVPQ 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APQQPPSTESSSSSSSSSTSQSSSTTPSTNNSTTTNPNNNTQQSNTTPDQQNQNPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VG-----AEVYVSANGTLTTDATSEGTVTKDPLKALDEAISSIDKFRSSLGAIQNRLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGNGLTVAAKVYRSMMTYL-----SEGSNPED--WNIPEGLYRNGEFVFKNGARSTWNSP 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTASAKYADNTDVSNATATYTDADGEMTTIGSYTTKYSIDANNGKVTVDSGTGSGKYAPK 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PMYIHKVVFSDGSEKE--FSNVGTRAMKETTAYMMTDMMKTVLTYGTGRNAYLAWLPQAG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAT-LDGLFKKAGDGQSIGFNKTASVTMGGTTYNFKTGAD-----AGAATANAG---- 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YKAASGEV -----TINDAGGA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VSFTDTASKETVLNKVAT--AKQGTAVAANGDTSATITYKSGVQTYQAVFAAGD
                                                                                                                                                                                                                                                                                                                                                    2843
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Groden, Joanna
Hedge, Philip John
Joslyn, Geoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinzler, Kenneth
Markham, Alexander Fred
Nakamura, Yusuke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thliveris, Andrew
                                                                                                                                                                                          4.2%; Score 146; DB ilarity 18.8%; Pred. No. 1.1; Conservative 98; Mismatches
                                                                                                                                                                                            213;
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                                                                                                                                                                                                                              Length 2843;
                                                                                                                                                                                          Indels 250;
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APPLICANT: GREENE, JONATHAN R.

TITLE OF INVENTION: CANDIDA ALBICANS NUCLEIC ACI
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 2976-4031
CURRENT APPLICATION NUMBER: US/10/179,131
CURRENT FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 10194
SEQ ID NO 6430
LENGTH: 1029
TYPE: PRT
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                                                                                                                                                                                                                                ; ORGANISM: Candida albicans US-10-179-131-6430
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                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1216 ENTSTPSSNAKRQNQLHPSSAQSRSGQPQKA 1246
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                     137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                586
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                                                           264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 476 YMMTDMMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYT 535
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                                                                                               77
YYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVLSEMKNQG---YISAEQ 193
                                                         IETTATSSVAGDISIAKKCSSKNGPKPILKKRTMEQSMISHSNLL-----KLQLATQI 316
                                                                                               IKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINKVYMSNGNYGMQTAAQN 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STTTNPNNNTQQSN----TTPDQQNQNPQPA 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERPTNYSIKYNEEKRHV-DQPIDYSLKYATDIPSSQKQSFSFSKSSSGQSSKTEHMSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYRNGEFVFKNGARSTWNSP-----APQQPPSTESSSSSSDSSTSQSSSTT-PSTNN 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SR-----GANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKPTNYSERYSEEEQHEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERNALR----RSSAAHTHSNTYNF----TKSENSNR----TCSMPYAKLEYKRS--SNDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----KYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTA 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YAPALEYGYYDSTATIVHDEPYNYPGTNTPVYNWDRGYFGNITLQYA-LQQSRNVPAVET 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGSLDSSRSEKDRSLERERG----IGLGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAYMDNYLKEVINQVEEETGYNLLTTGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDE-- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---FDTNRHDDNRSDNFNTGNMTVLSPY------LNTTV-----LPSSSSS
                                                                                                                                     141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNSVSSNDGYGKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGELDT 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----LQVASTIVDVSNGKVIAQLGARHQSSNVSFGINQAVETNRDWGST--MKPITD 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHAW, KAREN J.
SHIMER JR., GEORGE H.
KESSLER, MARCO
NOLLING, JORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZENG, QIANDONG
                                                                                                                                     Conservative
                                                                                                                                                       4.2%;
                                                                                                                                     106;
                                                                                                                                                   Score 145.5; I
Pred. No. 0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----YTESTDDKHLKFQPHFGQQECVSPYR 1103
                                                                                                                                     Mismatches
                                                                                                                                                                           DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                              ACIDS AND POLYPEPTIDES,
                                                                                                                                     233;
                                                                                                                                   Indels
                                                                                                                                                                         Length
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                                                                                                                                     267;
                                                                                                                                     Gaps
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Search completed: August 11, 2002, 04:32:42 Job time: 538 sec

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Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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2: pir2:*
3: pir3:*
4: pir4:*
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Copyright (c) 1993 - 2000
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ALIGNMENTS

penicillin-binding protein 1A [imported] - Streptococcus pneumoniae (strain TIGR C;Species: Streptococcus pneumoniae (c;Species: Streptococcus pneumoniae (c;Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001 C;Accession: G95042
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holt nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; M.A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumon A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95042
A;Status: preliminary
A;Rolecule type: DNA
A;Residues: 1-719 <KUR>
A;Residues: 1-719 <KUR>
A;Residues: 1-719 <KUR>
A;Residues: 1-719 <KUR> Qy C;Genetics: A;Gene: SP0369 C;Superfamily: penicillin-binding protein QΥ Вþ Qy Вþ 망 δÃ В δÃ В Qy A;Cross-references: GB:AE005672; PIDN:AAK74536.1; PID:g14971838; GSPDB:GN00164; TIGR:A;Experimental source: strain TIGR4 Query Match 100.0%; Best Local Similarity 100.0%; Matches 666; Conservative 0 354 301 294 241 234 181 174 121 114 61 54 VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR 360 SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR 0; Score 3484; DB 2; Pred. No. 4.6e-194; ; Mismatches 0; Length Indels Read, T.D.; Peterson, S.; H
M.R.; Radune, D.; Holtzappl 719; 0; Gaps 300 240 413 353 293 , B.A.; Morri pneumoniae. 0, Morris

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RESULT 2
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$28038
penicillin-binding protein la - Streptococcus prenicillin-binding protein la - Streptococcus prenicillin-binding protein la - Streptococcus preumoniae
C;Species: Streptococcus pneumoniae
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-19
C;Accession: $28038
R;Martin, C.; Sibold, C.; Hakenbeck, R.
EMBO J. 11, 3831-3836, 1992
A;Title: Relatedness of penicillin-binding protein, Reference number: $28031; MUID:93010977
A;Reference number: $28031; MUID:93010977
A;Accession: $28038
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-719 <MAR>
A;Residues: 1-719 <MAR>
A;Cross-references: EMBL: X67873; NID:947419; PII
C;Superfamily: penicillin-binding protein lB
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              GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
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Pred. No. 1.5e-193;
2; Mismatches 0;
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R;Martin, C; Sibold, C; Hakenbeck, R.
EMBO J. 11, 3831-3836, 1992
A;Title: Relatedness of penicillin-binding
A;Reference number: $28031; MUID:93010977
A;Accession: $28037
A;Status: translation not shown
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C;Species: Streptococcus pneumoniae
C;Species: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_
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A;Residues: 1-719 <MAP>
A;Cross-references: EMBL:X67872; NID:947417;
C;Superfamily: penicillin-binding protein 1B
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                              GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
                                                                   SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
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Pred. No. 2.6e
4; Mismatches
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2.6e-193;
nes 0;
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penicillin-binding protein 1A - Streptococcus pne
C;Species: Streptococcus pneumoniae
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-199
C;Accession: A42893
R;Martin, C.; Briese, T.; Hakenbeck, R.
J. Bacteriol. 174, 4517-4523, 1992
A;Title: Nucleotide sequences of genes encoding F
A and 1B.
A;Reference number: A42893; MUID:92325042
A;Accession: A42893
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-719 <MAR>
A;Cross-references: GB:M90527; NID:g153766; PIDN:
C;Superfamily: penicillin-binding protein 1B
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A42893
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                                                                   VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR
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                                                                                                                LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
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 KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD
                        GYFGNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESD
                                                                                                                                                              SEMKNOGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
                                                                                                                                                                                                                                                                                                      KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN
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Pred. No. 5.1e-193;
3; Mismatches 1;
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C;Superfamily:
C;Keywords: gly
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A; Residues: 1-719 <KUR>
A; Cross-references: GB: AE007317;
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A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C. A; Title: Genome of the Bacterium Streptococcus pneumoniae A; Reference number: A97872; MUID:21429245; PMID:11544234
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Pred. No. 5.1e
3; Mismatches
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A; Residues: 1-719 <MAR>
A; Cross references: EMBL:X67869; NID:g47411; PIDN:CAA48069.1;
C; Superfamily: penicillin-binding protein 1B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 17-Apr-1993 #sequence_revisi
C;Accession: S28034
R;Martin, C.; Sibold, C.; Hakenbeck,
EMBO J. 11, 3831-3836, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          penicillin-binding protein la - Streptococcus pneumoniae (strain 56742) (fragment) C;Species: Streptococcus pneumoniae (Streptococcus pneumoniae (S;Pate: 17-Apr-1993 *sequence_revision 17-Apr-1993 *text_change 26-May-2000
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31; Mismatches 22;
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$28032

penicillin-binding protein la - Streptococcus pneumoniae (strain C; Species: Streptococcus pneumoniae C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change: C; Accession: $28032

R; Martin, C; Sibold, C; Hakenbeck, R.

EMBO J. 11, 3831-3836, 1992

A; Title: Relatedness of penicillin-binding protein la genes from A; Reference number: $28031; MUID:93010977

A; Accession: $28032
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A; Residues: 1-719 <MAR>
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92.0%;
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Pred. No. 3.2e-180;
5; Mismatches 18;
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penicillin-binding protein la - Streptococcus pneumoniae (strain 45)
C;Species: Streptococcus pneumoniae
C;Species: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-1
C;Accession: S28031
R;Martin, C; Sibold, C; Hakenbeck, R.
EMBO J. 11, 3831-3836, 1992
A;Title: Relatedness of penicillin-binding protein la genes from di. A;Reference number: 828031; MUID:93010977
A;Accession: S28031
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-719 <MAR>
A;Cross-references: EMBL:X67868; NID:947405; PIDN:CAA48068.1; PID:9
C;Superfamily: penicillin-binding protein lB
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                                                                                    SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
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KQYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSKKEFSNVGTRAMKETTAYMMTD
                                           AYFGNITLQYALQQSRNVTAVETLNKVGLDRAKTFLNGLGIDYPSMHYANAISSNTTESN
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91.9%;
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; Pred. No. 4.2e-180;
32; Mismatches 22;
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                    VSFGTNQAVETNRDWGSAMKPITDYAPAIEYGVYDSTATMVNDIPYNYPGTSTPVYNWDR
                                                                                                                    VSFGINQAVETNRDWGSTMKPITDYAPALEYGYYDSTATIVHDEPYNYPGTNTPYYNWDR
                                                                                                                                                    TGMDVYTNVDQEAQKHLWDIYNSDQYVSYPDDDLQVASTVVDVSNGKVIAQLGARHQASN
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                                                                                                                                                                                                                                          VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL
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Conservative

36;

Indels

0;

Gaps

0;

Of.

360

533 480 473 420 413 300

293 240 233 180 173

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penicillin-binding protein la - Streptococcus pneumoniae (strain 670) (fragm C;Species: Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 26-May-2000 C;Accession: $28033 K; Hakenbeck, R. R. MBO J. 11, 3831-3836, 1992 A;Title: Relatedness of penicillin-binding protein la genes from different cA;Reference number: $28031; MUID:93010977 A;Accession: $28033 A;Status: translation not shown A;Molecule type: DNA A;Residues: 1-719 <MAR> A;Residues: 1-719 <MAR> A;Cross-references: EMBL:X67867; NID:g47409; PIDN:CAA48067.1; PID:g47410 C;Superfamily: penicillin-binding protein 1B
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                      93.0%;
91.9%;
Score 3241; DI
Pred. No. 5.5e
36; Mismatches
                      DB 2;
.5e-180;
                                            Length
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C; Species: Streptococcus pneumoniae
A; Variety: strain 2039
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 2:
C; Accession: S28035
C; Accession: S28035
R; Martin, C.; Sibold, C.; Hakenbeck, R.
EMBO J. 11, 3831-3836, 1992
A; Title: Relatedness of penicillin-binding protein la genes from A; Reference number: S28031; MUID:93010977
A; Reference number: S28031; MUID:93010977
A; Accession: S28035
A; Status: translation not shown
A; Molecule type: DNA
A; Residues: 1-719 < WARP
A; Residues: 1-719 < WARP
A; Cross-references: EMBL: X67870; NID:947413; PIDN:CAA48070.1; PID
A; Experimental source: strain 2039
C; Superfamily: penicillin-binding protein lB
C; Keywords: antibiotic resistance; penicillin resistance
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C; Species: Streptococcus pneumoniae
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Best Local
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                                                                                                                                             VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR
                                                                                                                                                                                   SEMKNOGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT
                                                                                                                                                                                                                                                                                                                                                                                                                             KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 60
                              KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD 480
                                                                        VYFGNITIQYALQQSRNVTAVETLNKVGLDRAKTFLNGLGIDYPSMHYANAISSNTTESN
                                                                                                                                                                                                                                                                                                   VYMSNGNYGMQTAAQNYYGKDLRELSLPQLALLAGMPQRPNQYDPYSHPEAALDRRNLVL
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                                                                                                                                                                                                                                                                                                                            VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL 180
                                                                                                                                                                                                                                                                                                                                                                                                               KIFDSKNELIADLGSERRVNAQANEIPTDLVKAIVSIEDHRFFDHRCVDTIRIIGAFLRN
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S28036

C;Speciles: Streptococcus pneumoniae (strain C;Speciles: Streptococcus pneumoniae
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
C;Accession: S28036
C;Accession: C; Sibold, C; Hakenbeck, R.
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A;Residues: 1-608 <MAR>
A;Cross-references: EMBL:X67871; NID:g4741
C;Superfamily: penicillin-binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBO J. 11, 3831-3836, 1992
A;Title: Relatedness of penicillin-binding
A;Reference number: S28031; MUID:93010977
A;Accession: S28036
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Local Similarity 96.8%;
nes 537; Conservative 1
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                                       KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD
                                                                                                 SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT 240
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                                                                                                                                                                                                                            TGMDVYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN 300
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Pred. No. 1e-1
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from

different

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26-May-2000

8250) (fragment)

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653

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penicillin-binding protein 1 - Streptococcus oralis
C;Species: Streptococcus oralis
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #
C;Accession: B41893
R;Martin, C; Briese, T; Hakenbeck, R.
J. Batteriol. 174, 4517-4523, 1992
   RESULT
G86692
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A;Reference number: A42893; MUID:92325042
A;Accession: B42893
A;Status: preliminary
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A; Residues: 1-637 <MAR>
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                                                                        MAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLSEGSNPEDWNI
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                                                            MAVWTGYSNRLTPIVGDGFYVAAKVYRSMMTYLSEDDHPGDWTM
                                                                                                                  DMMKTVLAYGTGRGAYLPWLPQAGKTGTSNYTDDEIENYIKNTGYVAPDEMFVGYTRKYS
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                                                                                                                                                                                                      DKKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMT
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87.5%;
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Pred. No. 1.2e-148;
9; Mismatches 33;
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penicillin-binding protein 2A homolog pbpA [imported] - Listeria
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 2
                                             RESULT
AD1311
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A; Molecule type: DNA
A; Residues: 1-664 <STO>
A; Cross-references: GB: AE005176; PID:g12723428;
A; Experimental source: strain IL1403
C; GenetLos:
A; Gene: ponA
C; Superfamily: penicillin-binding protein 1B
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R;Bolotin, A.; Wincker, P.; Mauger,
Genome Res. 11, 731-753, 2001
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C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar_2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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644 TALVK---
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                                                                                                                                                                                                                               TYFGSMTYKSALALSRNIPAVKTLINVGLDNSSKFVNGLGITLDPLEYSNAISSNS----
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                           EFVFKNGARSTWNSPAPQQPPSTESSSSSSSSSTSQSSS
                                                                       GYTRKYSMAVWTGYSNRLTPLVGNGLTVAAKVYRSMMTYLS-EGSNPEDWNIPEGLYRNG
                                                                                                                 ILQSVLTLPLSESVGSYAAVPGLAAAGKTGTSNYTDSEMDQITEKYGSLPGMVSPDENFV
                                                                                                                                            MMKTVLTY----GTGRNAYLAWLPQAGKTGTSNYTDEEI----ENHIKTSQFVAPDELFA 532
                                                                                                                                                                         KNGGASSEKMAAAYAAFSNGGIYTKPYYVSKVVFPDGRTVEYKPDRSRAMQASTAYIMTN
                                                                                                                                                                                        KKYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSNVGTRAMKETTAYMMTD
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                                                       GYTPQYSMAVWTGYSNRMTPIYGTSTQIATKVFSSMMTQLTPDPSSVATWTMPEGVSQEG
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52.1%;
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Pred. No. 2.6e-
05; Mismatches
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27-Nov-2001 monocytogenes

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C; Accession: AD1311
R; Claser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, F.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A; Title: Comparative genomics of Listeria species.
A. Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AD1311
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-827 <GLA>
A; Cross-references: GB:MC_003210; PIDN:CAC99970.1; PID:g16411345; GSPDB:GN00177
A:Fxperimental source: strain EGD-e
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                                                                                                                                                        AGYTTNYSIAVWTGYDDKKKYVSASEQKIAQRMFSKLMAHASAGKTTADFKMPSNVV---
                                                                                                                                                                                                                MVSDVLKDVLSIGTGTSAAVPGVPAAGKTGTTNIPPE-----FTSKYYYPSGAARDSWF
                                                                                                                                                                                                                                MMTDMMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAP-----DELF
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                                                                                                                                                                                                                                                                                                                                FGYKGPISVRQALYQSRNIPALKTLQAVGLDKSEEFVNKLGITYDEGQNVESNAIGANS-
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                                         704
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                                                                                               VPILKGSNPIARAAQGTSSDKVSYELFLSGTAPTKTASTPEDEKK
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1.2e-62;
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Voss, H.; Wehland
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Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1683
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AD1683
C;Species: Listeria innocua
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 2C;Accession: AD1683
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A; Residues: 1-826 <GLA>
A; Cross-references: GB: AL592022; PIDN: CAC97236.1;
A; Experimental source: strain Clip11262
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KVYMSDRVHGMQTAAEHYEGKNVKDLTLAETALLAGMPQSPNNYNPYDHPEAAKKRRDQV 256
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Peptidoglycan synthesis; A
Multifunctional enzyme.
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SEQUENCE 637 AA; 70891
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PBPA_STROR
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"Nucleotide sequences of genes encoding penicillin-binding from Streptococcus pneumoniae and Streptococcus oralis with homology to Escherichia coli penicillin-binding proteins la J. Bacteriol. 174:4517-4523(1992).

-I- FUNCTION: CELL WALL FORMATION.

-I- PATHMAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.

-I- SUBCELLULAR LOCATION: Secreted.
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Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Antibiotic resistance; Cell wall;
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LQ-SNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYIN 119
                                          KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN
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Pred. No. 3.5e-148;
9; Mismatches 33;
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MEDLINE=95113769;
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NCBI_TaxID=1423;
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1A/1B (PBP1) [Includes: Penicillin-
insensitive transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.--) (DD-transpeptidase)].
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P39793;
  STRAIN=168;
MEDLINE=98389671; PubMed=9721295;
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                                                                                                                                                                                                  Sorokin A.V.,
                                                                                                                                                                                                                           MEDLINE=96349105; PubMed=8760912;
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subtilis ponA operon, which codes for
(PBP) 1 and a PBP-related factor.";
J. Bacteriol. 177:326-335(1995).
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                                                 GROWTH REQUIREMENTS
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                                                                                                  hlysis of the Bacillus kdg loci cloned in a 142:2005-2016(1996).
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EMBL;
                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
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EMBL; L47838; AAB38459.1;
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                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                             entities requires a license agreement
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"Septal localization of pen:
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                                                                                                                                                                                                                                                                                                                                                          MISCELLANEOUS: CELLS LACKING THE PROTEIN REQUIRE INCREASED LEVELS OF MG2+ OR CA2+ FOR GROWTH AND GERMINATION. APPROXIMATELY 50% OF CELLS WITHOUT THE PROTEIN CONTAIL ABNORMAL FTSZ RINGS, SUGGESTING IT IS INVOLVED IN SEPTUM SYNTHESIS; INCREASED LEVELS OF MG2+ OR CA2+ ONLY PARTIALLY ELIMINATE THE SEPTATION DEFECTS. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE TRANSGLYCOSYLASE FAMILY.

SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE TRANSPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTO SPORE GERMINATION.

PTM: THE PRODUCT EXPRESSED FROM THE TRANSLATION APPEARS AS TWO BANDS ON A GEL (1A AND 1B), BUT TAGID SEQUENCE OF EACH PROTEIN IS UNKNOWN.

PTM: THE N-TERMINUS IS BLOCKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNITS) (BY SIMILARITY).

PATHWAY: FINAL STAGES IN PEDTIDOGLYCAN SYNTHESIS.

SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN, F

SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN, F

OVER THE WHOLE CELL AT LOW CONCENTRATIONS. ALSO I

DIVISION SITE IN VEGETATIVE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS A PENICILLIN-INSENSITIVE TRANSGLYCOSYLASE N-TERMINAL DOMAIN (FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE CHORUSTES).
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                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                      U11883;
                                                                         AAA64947.1; -.
AAB38459.1; -.
                                                       CAB14148.1;
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Pfam; PF00041; fn3; 1.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Transglycosyl; InterPro; InterPro; DOMAIN Peptidoglycan synthesis; Cell wall; Hydrolase; Multifunctional enzyme; Antibiotic SMART; SM00060; FN3; InterPro; PRANSMEM IPR003961; FN_III.
IPR001264; Transglycosyl.
IPR001460; Transpeptdse. resistance; 1 37 38 58 Transglycosyl; 1. Complete proteome.
CYTOPLASMIC enzyme; SIGNAL-ANCHOR ; Transferase; Transmembrane; (POTENTIAL) Glycosyltransferase;
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ACYLATED BY PENICILLIN

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SIMILARITY).

TRANSPEPTIDASE

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P38050;
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01-OCT-1994 (Rel. 30, Last
16-OCT-2001 (Rel. 40, Last
                 Penicillin-binding propper or PONA.
Bacillus subtilis.
Bacteria; Firmicutes;
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Bacillus/Staphylococcus
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                                                                                                                                                                                                                                                                                           NDQDKKQDNTNTNPSDNNNQDQSNDN-DNDNSNNQ 873
                                                                                                                                                                                                                                                                                                                                                                           {\tt KSTASTSYEVPKAEDDEDKKDQQQTDDEKQDDEKTQDDTQTDDSQKDDGQTDQDQTDDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YTPQYTAAVWTGMGENEAGKKSLSAEEQKVAKRIFAQLIADVDDGSGSFEKPD--SVVEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAYMMTDMMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGGFGGND--GVSPLTMAGAYSAFGNNGTYNEPHFVKSIEFNDGTKLDLTPKSKSAMSDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRNQPVG---GFNYATQTKAQPGSTIKPILDYGPVIENKKW-STYEQIDDSAYTY-SNGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARHOSSNVSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQSLTLSWNYDGDATFAVKQSVDGGSYSEIQNSSAKEAVISGVQPGSVYKFEVTAVSDDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDVDPSADGLKIYTTLDTKAQDKLDELMDGDT-VGFTEG-MQGGVTLLDTKNGEVRAIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IYFSPRAYGIGKAAEEFFGVTDLSKLTVEQAATLAGMPQSPTAYNPVKNPDKAEKRRNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSN-SLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IYDKNGKEIAEVGAEKRTYVSIDEIPDVVKEAFIATEDARFYEHHGIDPVRIGGALVANF 138
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                     Bacillus/Clostridium group;
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1F (PBP-1F).
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Pred. No. 4.2e-50;
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EMBL; L10630; AAA71942.1;
EMBL; M97208; AAA22516.1;
EMBL; M97208; CAB12851.1;
EMBL; 299109; CAB12851.1;
PIR; A40614; A40614.
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Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell wall;
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InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning and characterization of the Bacillus subtilis hemEHY gene cluster, which encodes protoheme IX biosynthetic enzymes.";
J. Bacteriol. 174:8081-8093(1992).
-j- FUNCTION: CELL WALL FORWATION. MAY BE INVOLVED IN OUTGROWTH OF THE GERMINATED SPORE OR IT COULD FUNCTION IN THE SYNTHESIS OF THE GERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98240224; PubMed=9579061;
Noback M.A., Holsappel S., Kiewiet R., Terpstra P., Wambutt R.,
Wedler H., Venema G., Bron S.;
"The 172 kb prkA-addAB region from 83 degrees to 97 degrees of the
                                                                                                                                                                                                         Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long 
modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93094140; PubMed=1459957; Hansson M., Hederstedt L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 122-714 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subtilis pbpF gene, which codes for a putative clas high-molecular-weight penicillin-binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microbiology
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                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Popham D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=93328693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriol. 175:4870-4876(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SY SUBCELLULAR LOCATION: Membrane-associated DEVELOPMENTAL STAGE: EXPRESSION REMAINS CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GROWTH, DECREASES DURING EARLY SPORULATION, FORESPORE DURING LATE SPORULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSGLYCOSYLASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                                          W.
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O66874;
O660874;
O6-OCT-2001 (Rel. 40, Created)
O660874;
O6-OCT-2001 (Rel. 40, Last sequence update)
O660874;
O67-2001 (Rel. 40, Last sequence update)
O67-2001 (Rel. 40, Last annotation update)
O680874;
O680874;
O780874;
                                                                                                                                                                                                          MEDLINE=98196666; PubMed=9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M.,
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aqu
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PBPA_AQUAE
O66874;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGMMNDQGYISAKEAVTAQGR--TLGLH-VKKQSETP-WFDSYIDLVIKEAEDKYSISGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILAGGKVEGGTTITQQLAKNIFL---THDKTFLRKTKEVIIAINLERDYSKDKLLEMYLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIVDQNGDEVASLYTENREPVSINEIPKQVREAFIAVEDKRFYEHHGIDAKSVGRAVYRD
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                                                                                                                                              392:353-358(1998).
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Pred. No. 2.7e-35;
9; Mismatches 23:
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Query Match Best Local S Matches 207

al Similarity 30.7 207; Conservative

20.4%;

109;

Score 712; DB 1 Pred. No. 1e-33; 9; Mismatches 2

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Indels

132;

Gaps

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SOUTH THE TENTON TO THE TENTON
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Interpro; IPRO01460; Transpeptidse.

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Pfam; PF00905; Transglycosyl; 1.

Probom; PD001895; Transglycosyl; 1.

PD001895; Transg
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
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                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                      ACYLATED BY PENICILLIN (B
37F756397C9D7B38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 TRANSPEPTIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSGLYCOSYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PERIPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
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Length 726;
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::|| | :| :| :| : | : | : | : | SDGSEKEFSNVG--TRAMKETTAYMMTDMMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTD VGKKVGLDNLKPYYSLAL-FLNGLGIDYPSIHYSNAISSNTTESDKKYGASSEKMAAAYAAFANGGTYYKFMYIHKVVF VS--IDVKTGEIKAIVGGR---SYAYSQFNRAVKALRQPGSAIKPVI-YLSALLKGMTQI ASTIVDVSNGKVIAQLGARHQSSNVSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDS GKIYVAKILKYDGNFMKVEIHGKKLKGEIKGLNTEGHKYVFVKYLGGNRAEIIPDLEGSL TTGMDVYTNVDQE----AQKHLWD-----LKRMLEEGYITPEQYEEAVNKPLT----VKKENKY-KFSDYFLDMVKSYVFNKYGEIAY LSEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLL YRAGRIYQGGSTITQQLAKNLFL---TRERTLERKIKEALLAIKIERTFDKKKIMELYLN EVYDAKGRLYGTIGIQKRFYVSIDKIPEHVINAFVATEDRNFWHHFGIDPVAIVRAAIVN EEIENHIKTSQFVAPDELFAGYTRKYSMAVWTGYSNRLTPLVG---NGLTVAAKVYRSMM ENGEVLE-ENVPECEEVLPKPETRVPVDMLRAVVLEGTARRASVLDRIVAGKTGT--KGRLKIYTTIDLDYQKIAQKSLEEGLKRVAKIIGLPFLPKSEEDMELAYEKEAQLKRLKR LQSNSL-QGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYIN -GTVE--VTPLQLTAAYQVFANLGTECKPFFIKKIVD -NTD----EYVAY----PDDELQV -TD 454 510 336 276 162 119 105 562 394 450 336 239 396 259

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PBPA_NEIFL
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A ROPP P. A., NICHOLAS R.A.;

"Nucleotide sequence of the ponA gene encoding penicillin-binding of protein 1 of Neisseria flavescens.";

"Drotein 1 of Neisseria flavescens.";

Submitted (Aug-1998) to the EMBL/GenBank/DDBJ databases.

C -!- FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED PEPTIDOGLYCAN FROM THE LIPID INTERWEDIATES. THE ENZYME HAS A COMMON THE LIPID INTERWEDIATES. THE ENZYME HAS A COMMON OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE TRANSCRIVED OF TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE COMMON OF THE PEPTI
                                                                                             Matches
                                                                                                                    Query Match
Best Local
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ACT_SITE
SEQUENCE
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087626;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1A (PBP-1a) (PBP1a) [Includes: Penicillin-
insensitive transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.--) (DD-transpeptidase)].
                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell wall; Transferase;
                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-NRL 30009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria flavescens.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRCA OR PONA.
                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
52
                                            N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSGLYCOSYLASE FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION;
TRANSPEPTIDASE FAMILY.
                                IYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNL
IYSSDGQVIGVYGEQRREFTKIDDFPKILKDAVIAAEDKRFYDHWGVDVWGVARAVIGNV
                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                       multifunctional enzyme; Transmembrane;
hor; Antibiotic resistance.
2YTOPLASMIC (POTENTI)
10 30 SIGNAL-ANCHOR (TYPE )
                                                                                                                                                                                                                  798
                                                                                             Conservative
                                                                                                                                                                                                                                                                                       31
50
                                                                                                                                                                                                          798
218
699
460
87703
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25.8%;
                                                                                             129;
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                                                                                                                 Score
Pred.
                                                                                                                                                                                                               TRANSPEPTIDASE.
ACYLATED BY PENICILLIN (E
ODDCDF6FD25953AA CRC64;
                                                                                                                                                                                                                                                                                  PERIPLASMIC (POTENTIAL)
TRANSGLYCOSYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subdivision;
                                                                                             Mismatches
                                                                                                                 680.5;
No. 7.5
                                                                                         1.5e-32;
nes 277;
                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
OR (TYPE II MEMBRANE
                                                                                                                                          DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycosyltransferase;
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                                                                                                                                          Length
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                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane;
                                                                                           179;
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                                                                                           Gaps
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RESULT 7
PREAL 7
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                                                                                                                                                                                                                                PBPA_PSEAE STANDARD; PRT; 822 AA.

(Q07806;
Q07806;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1A (PBP-la) (PBPla) (Includes: Penicillin-
insensitive transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.--) (DD-transpeptidase)].
  STRAIN-ATCC 19 Handfield J.,
                                                                                                                                                                 Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                             MRCA OR PONA OR PA5045.
                                                           SEQUENCE FROM
                                                                                                              NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMQDVVRVGTARGAATLGRSDIAGKTGTTN-----DN-
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                            DM N.A.
15692 / PAO1;
Gagnon L.,
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                                                                                                                                                                       subdivision;
     Huletsky
        Α.,
                                                                                                                                                                       Pseudomonadaceae
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QY
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                                                                                   Query Match
Best Local S
Matches 205
                                                                                                                                                                                         DOMAIN
ACT_SITE
SEQUENCE
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InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptdase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Martin P.R., Hobbs M., Free P.D., Jeske Y., Mattick
"Characterization of pilQ, a new gene required for t
type 4 fimbriae in Pseudomonas aeruginosa.";
Mol. Microbiol. 9:857-868(1993).
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Peptidoglycan synthesis; Cell wall; Transferase; Glycosyltransferase;
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  49
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PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SUBCELLULAR LOCATION: Type II membrane
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SIMILARITY: IN THE
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KVYSEDGKLISEFGEMRRTPIRFADIPQDFIHALLSAEDDNFANHYGVDVKSLMRAAAQL
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                                                                                                         Similarity
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SEQUENCE FROM N.A.
STRAIN=NRL 3716;
ROPP P.A., Nicholas R.A.;
ROPP P.A., Nicholas R.A.;
PNucleotide sequence of the ponA gene encoding protein 1 from Neisseria lactamica.";
                                                                                                           Neisseria
Bacteria;
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Proteobacteria;
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(Rel. 40, Last annotation update)
kinding protein 1A (PBP-1a) (PBP1a) [Includes: Penicillin-
transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
sensitive transpeptidase (EC 3.4.-.-) (DD-transpeptidase)].
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-!- FUNCTION: CELL W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell wall; Transferase;
Hydrolase; Multifunctional enzyme; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
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InterPro; IPR001460; Transpeptdse.
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398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local 203;
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- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SY
- SUBCELLULAR LOCATION: Type II membrane pr
similarity).

- SIMILARITY: IN THE N-TERMINAL SECTION: BE
TRANSGLYCOSYLASE FAMILY.

- SIMILARITY: IN THE C-TERMINAL SECTION: BE
TRANSPEPTIDASE FAMILY.
                                                                                                                                                                                                                   229
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FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED
PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS A
PENICILLIN-INSENSITIVE TRANSGLYCOSYLASE N-TERMINAL DOWAIN
(FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE
TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European
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                                                                                                                                                                                                                                                                                       VYSADGKIIGIYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYQHWGVDVWGVARAVVGNI
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                                                                                                         -KHLWDIYNTDEYV--
                                                                                                                                                                               TGYNLLTTGMDVYTNV-----
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                                                                     SQYLSGLYTVDKMVPAVVLDVTKKKNVVTQLPGGKRVTLDRRALGFAARAVDNEKMGEDR
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SIGNAL-ANCHOR
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les 265;
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                                                                                                                                                                                                                                                                           Parkhill J., Achtman M., James K.D., Bentley S.D., Churche: Klee S.R., Morelli G., Basham D., Brown D., Chillingworth Y. Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., I Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.; "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491."; Nature 404:502-506(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ol-MAR-2002 (Rel. 41, Last annotation update)
Penicillin-binding protein IA (PBP-Ia) (PBPIA) [Includes: Penicillin-
insensitive transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.-.-) (DD-transpeptidase)].
MRCA OR PONA OR NMAD655 OR NMB1807.
Neisseria meningitidis (serogroup A), and
Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisserfaceae; Neisseria.
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., N
Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J
Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dough
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Cl
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan
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16-OCT-2001 (Rel. 40, Last
01-MAR-2002 (Rel. 41, Last
                                                                                                                                                                   STRAIN=MC58 / Serogroup MEDLINE=20175755; PubMed
                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Z2491 / Serogroup A / Serotype
MEDLINE=20222556; PubMed=10761919;
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meningitidis.";
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MEDLINE=97252514; PubMed=
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Matches 203
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ACT_SITE
SEQUENCE
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pfam; PF00912; Transglycosyl; 1.

pfam; PF00905; Transpeptidase; 1.

proDom; PD001895; Transglycosyl; 1.

proDom; PD001895; Transglycosyl; 1.

Proptidoglycan synthesis; Cell wall; Transferase; Glycosy; Hydrolase; Multifunctional enzyme; Transmembrane; Inner r Signal anchor; Antibiotic resistance; Complete proteome.

Signal anchor; Antibiotic resistance; Complete proteome.

DOMAIN

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CYTOPLASMIC (POTENTIAL).

TRANSMEM

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SIGNAL-ANCHOR (TYPE II MEMB
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PATHWAY: FINAL STAGES IN P
SUBCELLULAR LOCATION: Type
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SIMILARITY: IN THE C-TERMINAL
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SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collable of the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
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                                                                                                                                    SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDN-----
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AE002530; AAF42144.1;
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03; Conservative
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J. Bacteriol. 179:2783-2787(1997).

J. Bacteriol. 179:2783-2787(1997).

J. Bacteriol. CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED PEPTIDGCLYCAN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS A PENICILLIN-INSENSITIVE TRANSGLYCOSYLASE N-TERMINAL DOMAIN (PORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE SUBUNITS) (BY SIMILARITY). ESSENTIAL FOR CELL WALL SYNTHESIS.

-!- PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.

-!- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penictllin-binding protein 1A (PBP-la) (PBPla)
insensitive transglycosylase (EC 2.4.2.-) (Pept
                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                            *Cloning and characterization
                                                                                                                                                                                                                                                                                                                            Ropp P.A., Nicholas R.A.;
                                                                                                                                                                                                                                                                                                                                        MEDLINE-97252514; PubMed-9098083;
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                                                                        SIMILARITY: IN THE N-TE TRANSGLYCOSYLASE FAMILY SIMILARITY: IN THE C-TE
                                                                                                                      similarity).
                                                           TRANSPEPTIDASE FAMILY
                           SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KERMYTDPGLTLDNSGTAPQPSRRAKEDDGGAAEGGRQAADDEVRQDMQETPVLPSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YITLRQALTASKNMVSIRILMSIGVGYAQQYIRRFGFRSSELPASLSMALGTGET-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMRQPGSTEKPEV-YSAALSKGM--TASTVVNDAPISLPGKGPNGSVWTP-KNSDGRYSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TURDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTN-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKIMQDVVRVGTARGAAALGRTDIAGKTGTTN-----DN-----KDAWFVGFNPD
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                                                                                                                                                                                                                                                                                             protein 1 from Neisseria
                                                                                                                                                                                                                                                                                                                                                                       FROM
                                                                                                                                                                                                                                                                                                                                                     AND ATCC 700825 / FA 1090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transpeptidase
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                                                                                                                                                                                                                                                                                          the ponA gen
gonorrhoeae
                                                                         SECTION;
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InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell wall; Transferase; (Hydrolase; Multifunctional enzyme; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Local Similarity 26.4%;
nes 207; Conservative 12
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DVVRVGTARGAAALGRTDIAGKTGTTN-----
                               TVLTYGTGRN-AYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYSMAV
                                                                                                     MAAAYAAFANGGTYYKPMYIHKVVFSDGSEKE----
                                                                                                                                       QALTASKNMVSIRILMSIGVGYAQQYIRRFGFRPSELPASLSMALGTGET---
                                                                                                                                                                        YALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESDKKYGASSEK
                                                                                                                                                                                                                                                                                 VIRVKNNGGRWAVVQEPLLQGALVSLDAKTGAVRALVGGYDFHSKT---FNRAVQAMRQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAEAYSVFANGGYRVSSHVIDKIYDRDGRLRAQMQPLVAGQNAPQAIDPRNAYIMYKIMQ
                                                                                                                                                                                                             GSTFKPFV-YSAALSKGM--TASTVVNDAPISLPGKGPNGSVWTP-KNSDGRYSGYITLR
                                                                                                                                                                                                                                                GSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTN----
                                                                                                                                                                                                                                                                                                                                                          GLYTVDKMVPAVVLDVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIRRGA
                                                                                                                                                                                                                                                                                                                                                                                             DIYNTDEYV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LTTGMDVYTNVDQEAQK---------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEMKNQGYISAEQYEKAVNTPI--TDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSGSVQSGASTITQQVAKNFYLS---SEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRNL
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797
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Pred. No. 2.9e-29;
0; Mismatches 287
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TRANSPEPTIDASE.
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-DN------KDAWFVGFNPDVVTAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                  -- FSNVGTRAMKETTAYMMTDMMK
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R (TYPE II MEMBRANE
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for
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Ropp P.A., Nicholas R.A.;

Ropp P.A., Nicholas R.A.;

"Cloning and sequence analysis of the ponA gene encoding penicillin binding protein 1 from Neisseria cinerea.";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED - PEPTIDOGLYCAN FROM THE LIFID INTERMEDIATES, THE ENZYME HAS A PENICILLIN-INSENSITIVE TRANSGLYCOSYLASE N-TERMINAL DOMAIN (FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE
                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                             ProDom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell wall; Transferase;
Hydrolase; Multifunctional enzyme; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                  EMBL; AF085340; AAC34128.1; ...
InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                           Pfam; PF00905; Transpeptidase; 1.
                                                                                                                                                                                                                                                                                                                                  Pfam; PF00912; Transglycosyl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send
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Penicillin-binding protein IA (EPB-1a) (PBP1a) [Includes: Penicillin-
insensitive transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.-.-) (DD-transpeptidase)].
                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                        Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria cinerea.
Bacteria; Proteobacteria;
                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SIMILARITY:
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PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SUBCELLULAR LOCATION: Type II membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: IN THE C-T TRANSPEPTIDASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          an email to license@isb-sib.ch).
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ACYLATED BY PENICILLIN
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SIGNAL-ANCHOR
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SEQUENCE FROM N.A. STRAIN=EL TOR N16961 / SEROTYPE 01 MEDLINE=20406833; PubMed=10952301;
                                                                                                       Q9KNUS;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1A (PBP-la) (PBPla) [Includes: Penicillin-insensitive transglycosylase (EC 2.4.2.-) (Peptidoglycan TGase);
Penicillin-sensitive transpeptidase (EC 3.4.-.-) (DD-transpeptidase)].
                                                                                 Vibrio cholerae
                                                      NCBI_TaxID=666;
                                                                      Bacteria; Proteobacteria;
                                                                                                 MRCA OR PONA OR VC2635
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                                                                                                                                                                                                                                                                                                                                    KIMQDVVRVGTARGAAALGRSDIAGKTGTTN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRRGSVIRVRNNGGRWVVVQEPLLQATLVSLDAKTGAVRALVGGYDFHSKT----FNRAAQ
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Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Ve
Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE004330; AAF95776.1; ALT_INIT.TIGR; VC2635; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Probom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell wall; Transferase; Glycosyltransferase;
Hydrolase; Multifunctional enzyme; Transmembrane; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 406:477-483(2000).
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                                                                                                                                                  \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS A PENICILLIN-INSERSITIVE TRANSGLYCOSYLASE N-TERMINAL DOMAIN (FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE TRANSPEPTIDASE C-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE SUBUNITS) (BY SIMILARITY).

PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS.
SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane (SIMILARITY).

SIMILARITY: IN THE N-TERMINAL SECTION: BELONGS TO THE TRANSGLYCOSYLASE FAMILY. IN THE G-TERMINAL SECTION: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSGLYCOSYLASE FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSPEPTIDASE FAMILY.
KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                           LASGSASQGASTITQQLARNFFLS---NEKKVMRKVKEIFIAIHIEQLLSKQEILELYLN
                                                                               LQSNSL-QGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYIN 119
                                                                                                                      QVFSQDGKLIAQFGEKRRIPLKLEEMPKELIEAVIATEDSRYYEHYGFDPIGITRAAFAV 108
                                                                                                                                                                                al Similarity
200; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001264; Transglycosyl.
                                                                                                                                                                                                                                                           825
                                                                                                                                                                                                                                                                         28
48
413
471
                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                               Antibiotic resistance; Complete proteome.

1 6 CYTOPLASMIC (POTENTIAL).
7 27 SIGNAL-ANCHOR (TYPE II MEMBRANE
                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                         825
216
752
471
                                                                                                                                                                                                                                                           91986
                                                                                                                                                                                               17.7%;
24.3%;
                                                                                                                                                                                 128;
                                                                                                                                                                                                                                                         WW;
                                                                                                                                                                                Score 617; DB
Pred. No. 3.6e
28; Mismatches
                                                                                                                                                                                                                                                                         ACYLATED BY PENICILLIN
                                                                                                                                                                                                                                                                                     TRANSPEPTIDASE
                                                                                                                                                                                                                                                                                                      TRANSGLYCOSYLASE
                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                           8A9553DA2650B9D2
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                                                                                                                                                                                               DB 1;
.6e-28;
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                                                                                                                                                                                                                                                           CRC64;
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                                                                                                                                                                                                                                                                         SIMILARITY).
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                                                                                                                                                                                 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collaboration -
L outstation -
                                                                                                                                                                                                                                                                                                                                                  PROTEIN)
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RESULT
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                                                                                                                                                                                                                                                                                                                         protein
J. Bacte
                                   Oudega B., Koningsteijn G., Van Zoest A.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Membrane-associated (Probable).
-!- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING VEGETAT
-!- DEVELOPMENTAL STAGE: EXPRESSION INTO SPORULATION.
-!- PTM: THE N-TERMINUS IS BLOCKED.
-!- PTM: THE N-TERMINUS IS BLOCKED.
                                                                                                                             STRAIN-168;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
STRAIN=168;
                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                             BACSU
              ÷
                                                                                                                                                                                          "Cloning, nucleotide sequence, mutagenesis, and mapping of the Bacillus subtilis pbpD gene, which codes for penicillin-binding
                                                                                                                                                                                                                   Popham D.L.,
                                                                                                                                                                                                                                 MEDLINE=95050302; PubMed=7961491;
                                                                                                                                                                                                                                                                                 Bacillus/Staphylococcus
NCBI_TaxID=1423;
                                                                                                                                           SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              787
                                                                                                                                                                   Bacteriol.
             D-ALANYL-D-ALANINE CARBOXYPEPTIDASE 2 FAMILY CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLTVAAKVYRSMMTYLSEGSNPEDW---NIPEGLY--RNGEFVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --YNTDE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTGWNG-TGWRAQALKRRDIGGKTGTTNDSKDAWYNGYAPGIVGVAWVGFDDHSRNLGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSNAISSNTTESDKKYGASS---EKMAAAYAAFANGGTYYKPMYIHKVVFSDGSEKEFSN 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---KFNRATQSVRQVGSSIKPFI-YSAALNKGL--TLATLINDAPIN------QWDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLDSS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APNRNIEDDVSGAESGGKTALPAWVEFMSLALQDVPVQQKAVPNNIARVRIDRDTGLLTN 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEFSAEPKVVCHRECSSELDEFAEQDAASPYAPKVISEQNAFLTREMLYSNIWGGGEWSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSFGINQAVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTNTPVYNWDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SANEFLAAGQQIWVRPRTQDGAITAWKLTQVPNANTAFVAMNPENGAVTALVGGFNFVHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -TGRNAYLAWLPQA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQGTAWRPKNSPPTYTGPTRLRIGLAQSKNVMAVRVLREVGLDETREYLTRFGFKLDQLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQFVAPDELFAGYTRKYSMAVWTGYS-----
                                                                                                                                                                               4.";
              IT IS UNCERTAIN WHETHER MET-1 OR MET-3
                                                                                                                                                                                                                     Setlow P.;
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                                                                                                                                           N.A.
                                                                                                                                                                   176:7197-7205(1994)

    SMFEYFEAGTEPTEYVSEHVNESIYSTSSGEELF

                                                                                                                                                                                                                                                         AND SEQUENCE
                                                                                                                                                                                                                                                                                               Bacillus/Clostridium us group; Bacillus.
                                                                                                                                                                                                                                                                                              group;
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Matches
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U11882; AAA64943.1;
EMBL; Z93933; CAB07915.1;
EMBL; Z99120; CAB15138.1;
MEROPS; S12.001; _-.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pfam; pF00912; Transglycosyl; 1.
pfam; pF00905; Transpeptidase; 1.
proDom; PD001895; Transglycosyl; 1.
peptidoglycan synthesis; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SubtiList; BG10977; pbpD.
InterPro; IPR001264; Transglycosyl
InterPro; IPR001460; Transpeptdse.
576
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                                                                                                                                                                                    DSTATIVHDEPYNYPGTNTPVYNWDRGYFGNITLQYALQQSRNVPAVETLNKVGLNRAKT 394
                                                                                                                                                                                                                                                                                                                        NKVYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                NLQSNSL-QGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYI 118
                                                                   KVVFSDGSE-KEFSNVGTRAMKETTAYMMTDMMKTVLTYGTGRNAYLAWLPQAGKTGTSN
                                                                                                                                 FLNGLGIDYPSIHYSNAISSN---
                                                                                                                                                            TTSSTI----DASKFCSKDYCPQNYNNRTYGTVTLDTAFKNSYNTPAIRMLDRVGIQKAFS
                                                                                                                                                                                                                QGGAAVINHQTHQIIALSGGKNYQ --- KYDFNRAYQAYRQPGSSIKPLLDYGPYIEQTGA
                                                                                                                                                                                                                                 QVASTIVDVSNGKVIAQLGARHQSSNVSFGINQAVETNRDWGSTMKPITDYAPALEYGVY
                                                                                                                                                                                                                                                                 RLQKASGKQKEKIENELSARVSTLMKDGVKIYTALDPYMQNQV--VAQMNSKLPYAD--V
                                                                                                                                                                                                                                                                                                                                                    VLSEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                YTDEETENHIKTSQFVAPDELFAGYTRKYSMAVWTG---
                                                                                                        YIE-----PYHFAKLVDSDYLLPAALGGFTNGMTPLEMTKAYTTFGNSGSYTPSHAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity 26.9
159; Conservative
                                                  KVTDLKGKTLYKWNDKATQIFSVRTNMQLKKLMSSVVKSGTGKKAYFNAPYIGGKTGTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteome.
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624 AA;
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624
388
70625 1
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 DMWFVGLTDTYTMGVWVGKDTPTSVEYLHSISP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.

PENICILLIN-BINDING PROTEIN
ACYLATED BY PENICILLIN (BY
ACYLATED BY PENICILLIN (BY);
B0E6BD4B4EC7ACE4 CRC64;
                                                                                                                                 -TTESDKKYGASSEKMAAAYAAFANGGTYYKPMYIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        598.5; DI
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                            -YSNRLTP
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SIMILARITY).
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RESULT 14 PBPA_HAEIN

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SEQUENCE FROM N.A.

STRAIN-RD / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed-7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fieldes C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Weidman J.F., Phillips C.A., Spriggs T., Bedblom E., Cotton R.C., The Cotton M.D., Weidman J.F., Phillips C.A., Spriggs T., Bedblom E., Cotton R.C., Spriggs T., Bedblom E., Cotton R.C., The Cotton M.D., Weidman J.F., Phillips C.A., Spriggs T., Bedblom E., Cotton M.D., Weidman J.F., Fanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., The Cotton M.S.M., The M.S.M., The Cotton M.S.M., The Cotton M.S.M., The M.S.M
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Sharma U.K., Dwarakanath P., Banerjee N.,
"Expression and characterization of the potal Haemophilus influenzae: functional complements of the potal complements of
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MEDLINE=92009183; PubMed=1916268;
Tomb J.-F, El-Hajj H., Smith H.O.;
"Nucleotide sequence of a cluster of gene
transformation of Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION BY MASS SPECTROMETRY. MEDLINE-20137488; PubMed-10675023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                system."
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en the Swiss Institute of Bioinformatics
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99;
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Pred. No. 1.1e
99; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
PERIPLASMIC (POTENTIAL).
TRANSGLYCOSYLASE.
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                                          464
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                                                                                                                                                                                                                                                                                                                INQAVETNRDWGSTMKPITDYAP
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                                                                                                                                                                              DR
                                                                                                                                                                              YDGPMRLRVGLGQSKNII
                                                                                         LGAASFTPLEMARAYAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 127;
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RESULT 15 PBPB_VIBCH

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Query Match
Best Local S
Matches 175
                                                                                     DOMAIN
ACT_SITE
SEQUENCE
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Q9KUCO;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Melson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Fraser C.M.;
                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                              EMBL; AE004145; AAF93769.1; TIGR; VC0602; -
                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 406:477-483(2000).

Nature 406:477-483(2000).

-i- FUNCTION: CELL WALL FORMATION. SYNTHESIS OF CROSS-LINKED
-i- PEPTIDOGLYCAN FROM THE LIPID INTERMEDIATES. THE ENZYME HAS A
PENICILLIN-INSENSITIVE TRANSGLYCOSYLASE N-TERMINAL DOMAIN
(FORMATION OF LINEAR GLYCAN STRANDS) AND A PENICILLIN-SENSITIVE
TRANSPEPTIDASE C.-TERMINAL DOMAIN (CROSS-LINKING OF THE PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Penicillin-binding protein 1B (PBP-1b) (PBP1b) (Murein polymerase)
[Includes: Penicillin-insensitive transglycosylase (EC 2.4.2.-)
[Pepiidoglycan TGase); Penicillin-sensitive transpeptidase
                                                                                                                                                                                                                                         Pfam; PF00912; Transglycosyl; 1.
Probom; PD001895; Transglycosyl; 1.
Peptidoglycan synthesis; Cell wall; Transferase; (
Peptidoglycan synthesis; Cell wall; Transmembrane;
Hydrolase; Multifunctional enzyme; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
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                                                                                                                                                                                            TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Creat
16-OCT-2001 (Rel. 40, Last
16-OCT-2001 (Rel. 40, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                            gnal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: IN THE N-TERMINAL SECTION;
TRANSGLYCOSYLASE FAMILY.
SIMILARITY: IN THE C-TERMINAL SECTION;
TRANSPEPTIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNITS) (BY SIMILARITY).

PATHWAY: FINAL STAGES IN PEPTIDOGLYCAN SYNTHESIS SUBCELLULAR LOCATION: Type II membrane protein.
   175;
                 Similarity
                                                                                                                                                                                                                                                                                                              IPR001264; Transglycosyl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOR N16961
   Conservative
                                                                                                                       162
415
                                                                                                                                                                                                       Antiblotic resistance; Complete proteome.

1 30 CYTOPLASMIC (POTENTIAL).
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PubMed=10952301;
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                     16.8%;
29.7%;
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 117;
                                                                                       MW;
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 Score 584; DB 1; 1
Pred. No. 2.6e-26;
7; Mismatches 241;
                                                                                                                                                                                     CYTOPLASMIC (POTENTI SIGNAL-ANCHOR (TYPE
                                                                                                 TRANSCLYCOSYLASE.
TRANSPEPTIDASE.
ACYLATED BY PENICILLIN (BY SIMILARITY).
                                                                                                                                                       (POTENTIAL).
PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                          Transferase; Glycosyltransferase; Transmembrane; Inner membrane;
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                                Length 777;
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   56;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNL-LTTGMDVYTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINKVYMSNGN----YGM
TTIWLGRDDNQPTKL--TGASGALRVYAQYLKYRIPEKLQLPW--PEGI
                                              MAVWTGY-SURLTPLVGUGLTVAAKVYRSMMTYLSEGSUPEDWUIPEGL 587
                                                                                                                                            MKTVLTYGTGR---NAYLAWLPQAGKTGTSNYTDEEIENHIKTSQFVAPDELFAGYTRKYS
                                                                                                                                                                                                                                           GASSEKMAAAYAAFANGGTYYKPMYIHKVVFSDGS--EKEFSNVGTRAMKETTAYMMTDM
                                                                                                                                                                                                                                                                                            GEVPLYLALAQSLNVPTVALGMKLGIDQVSATLGKLGVNRDEI---RPVPSMLLGS---F
                                                                                                                                                                                                                                                                                                                                          GNITLQYALQQSRNVPAVETLNKVGLNRAKTFLNGLGIDYPSIHYSNAISSNTTESDKKY
                                                                                                                                                                                                                                                                                                                                                                                           VLNASRQIGSLVKPAV-YLTALAHPDQYNLATTLEDKPLTLKGSEGSAWTP-RNYDRQYR
                                                                                                                                                                                                                                                                                                                                                                                                                                      AVETNRDWGSTMKPITDYAPALEYGVYDSTATIVHDEPYNYPGTN----TPVYNWDRGYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DQEAQKHLWDIYNTD--EYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSNVSFGINQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLASRLYFGQPLQELRIDQLALLVGMVKGPSYYNPMRYAERARERRDLVLKLMMEHDILT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLAKNIFLS----SDRTLWRKLREAYMALTIDYRYSKDRILEAYLNEVYLGQSGADAIHGF
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                                                                                              MKQGVQEGTGRYLNAQFSSAALAGKTGTTN-----DNR-----DSWFVGVDGREV
                                                                                                                                                                                             SLTPYQVAQMYQTLTNSGKKAPLSALRSVLDLEGNVLYESLPRV-SQAVDQQAAWLTTYA
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Search completed: Job time: 577 sec August 11, 2002, 04:35:11

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Result
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Maximum Match 1008
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Perfect score:
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebra

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle

9: sp_bhage:*

10: sp_plant:*

11: sp_virus:*

12: sp_virus:*

13: sp_vertebra

14: sp_unclassi

15: sp_archeap:

16: sp_bacteria:*

17: sp_archeap:
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          Q9reu0
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	34.5	41.6	41.7	44.7	44.9	45.0	45.1	45.1	45.4		47.6	•	50.4	53.8	54.0	54.9	55.1	55.3	55.6	•			58.5		60.0		77.4	80.1	80.9
	826	310	310	310	310	310	310	310	310	310	664	778	400	398	398	793	398	398	398	398	398	398	721	398	398	527	727	728	808
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i	Q92AB6	052744	Q93N72	052742	052740	052738	052737	052739	052743	052741	Q9CI23	Q9EXN1	087106	087104	087107	Q9EXM9	Q9R7M8	087103	Q9R7M7	087105	087108	Q9R7M5	Q99YL1	087102	Q9R7M6	070037	Q9F2G4	Q9F2G7	Q54951
	Q92ab6 listeria in	O52744 streptococc	Q93n72 streptococc		052740 streptococc	052738 streptococc			052743 streptococc	052741 streptococc	Q9ci23 lactococcus	Q9exn1 enterococcu	O87106 streptococc	O87104 streptococc	087107 streptococc	Q9exm9 enterococcu		087103 streptococc	Q9r7m7 streptococc	087105 streptococc	087108 streptococc	Q9r7m5 streptococc	Q99yll streptococc	O87102 streptococc		. 070037 streptococc	Q9f2g4 streptococc	Q9f2g7 streptococc	Q54951 streptococc

ALIGNMENTS

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                                             Query Match
Best Local Similarity
Matches 666; Conserv
                                                                                                                                                                                                                                                                                                                                              Ferroni A., Berche P.;
"Alterations to penicillin-binding proteins 1A, 2B and 2X amongst penicillin-resistant clinical isolates of Streptococcus pneumoniae serotype 23F from the nasopharyngeal flora of children.";

J. Med. Microbiol. 50:828-832(2001).
EMBL; AF210745; AAF17255.1;
InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transpleptdse.
pfam; pF00912; Transpleptdase; 1.
pfam; pF00915; Transpleptdase; 1.
prodom; pD001895; Transpleptdase; 1.
prodom; pD001895; Transpleptdase; 1.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=SP 1261;
                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae
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                                                                                                                                                                                                                                                      MEDLINE=21432820; PubMed=11549185;
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1313;
                                                                                                                                                                                                                                                                                                                  Streptococcus
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54
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           KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 60
KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDTIRILGAFLRN 113
                                              Conservative
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                                            Score 3484; DB 2;
Pred. No. 2.1e-181;
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"Alterations to penicillin-binding proteins 1A, 2B and 2 penicillin-resistant clinical isolates of Streptococcus serotype 23F from the nasopharyngeal flora of children." J. Med. Microbiol. 50:828-832(2001).

EMBL; AF210746; AAF17256.1; ...
InterPro; IPR001264; Transglycosyl.
InterPro; IPR001264; Transglycosyl: 1.
Pfam; PF009012; Transpeptidase; 1.
Probom; PD001895; Transglycosyl; 1.
                                                                                                                                                                                                                                                                                                 Streptococcus.
NCBI_TaxID=1313;
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O1-mAY-2000 (TrEMBLrel. 13,
O1-mAY-2000 (TrEMBLrel. 13,
O1-DEC-2001 (TrEMBLrel. 19,
PENICILLIN-BINDING PROTEIN:
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Best Local
Matches 66
                            PBP1A.
Streptococcus pneumonio
Bacteria; Firmicutes; 1
Streptococcus.
NCBI_TaxID=1313;
                                                                 O9RET3 PRELIMINARY;
Q9RET3;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-DEC-2001 (TrEMBLrel. 19, L
PENICILLIN-BINDING PROTEIN 1A
SEQUENCE FROM N.A
STRAIN=BM 4200;
MEDLINE=21432820;
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 PubMed=11549185;
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"Alterations to penicillin-binding proteins 1A, 2B and 2X a

"Alterations to penicillin-binding proteins 1A, 2B and 2X a

penicillin-resistant clinical isolates of Streptococcus pne

serotype 23f from the nasopharyngeal flora of children.";

L. J. Med. Microbiol. 50:828-832(2001).

R. EMBL; AF210752; AAF17262.1; -.

R. InterPro; IPR001264; Transglycosyl.

R. InterPro; IPR001460; Transpeptdse.

Pfam; PF00912; Transglycosyl; 1.

Pfam; PF00905; Transpeptdase; 1.

PF6m; PF00905; Transpeptdase; 1.

PF6m; PF00905; Transpeptdase; 1.

PRODOM; PD001895; Transglycosyl; 1.

SQ SEQUENCE 719 AA; 79781 MW; DB593F6BD47F72D CRC64;
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SEQUENCE FROM N.A.

C. STRAIN-PO-342, PO-273, AND PO-341;

COffey T.J., Daniels M., Enright M.C., Spratt B.G.;

Refortype 14 variants of the Spanish penicillin-resistant serotype is clone of Streptococcus pneumoniae arose by large recombinational replacements of the cpsA-pbpla region.";

Refortype 14 variants of the Spanish penicillin-resistant serotype is replacements of the cpsA-pbpla region.";

Refore of Streptococcus pneumoniae arose by large recombinational replacements of the cpsA-pbpla region.";

Reforming 10:00 (1999).

Refore in the post of the cpsA-pbpla region.";

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InterPro; IPR001460; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transpeptidase; 1.
ProDom; PD001895; Transglycosyl; 1.
SEQUENCE 719 AA; 79662 MW; A7B9
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Ferroni A., Berche P.;
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Last sequence
Last annotation
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Pred. No. 3.7e-172;
7; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A7B96EA15434A805 CRC64;
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                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coffey T.J., Daniels M., Enright M.C., Spratt B.G.;
"Serotype 14 variants of the Spanish penicillin-resistant serotype
clone of Streptococcus pneumoniae arose by large recombinational
replacements of the cpsA-pbpla region.";
Microbiology 145:0-0(1999).
EMBL; AF139889; AAD43073.1; -.
EMBL; AF13988; AAD43070.1; -.
EMBL; AF13988; AAD43072.1; -.
EMBL; AF13988; AAD43072.1; -.
EMBL; AF13988; AAD43072.1; -.
EMBL; AF159448; AAD48430.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-URU-E159, M134, URU-E135, AND URU-E157; Coffey T.J., Daniels M., Enright M.C., Spratt B.G.; "Serotype 14 variants of the Spanish penicillin-resistant clone of Streptococcus pneumoniae arose by large recombina replacements of the cpsh-pbpla region."; Microbiology 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9WW11 PRELIMINARY; PRT; 719 AA.
Q9WW11;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence up)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation
PENICILLIN-BINDING PROTEIN 1A.
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001264; Transglycosyl
InterPro; IPR001460; Transpeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-URU-E206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                           LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK
                                                   LQSNSLQGGSTLTQQLIKLTYFSTSTSDQTISRKAQEAWLAIQLEQKATKQEILTYYINK
                                                                                                                                                          KIYDNKNQLIADLGSERRVNAQANDIPTDLVKAIVSIEDHRFFDHRGIDSIRILGAFLRN
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                                                                                                                                                                                                                                                                                                                                                                                          PF00912; Transglycosyl; 1.
PF00905; Transpeptidase; 1.
m; PD001895; Transglycosyl; 1.
NCE 719 AA; 79701 MW; 3EDC
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22; Conservative
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                                                                                                                                                               "Alterations to penicillin-binding proteins 1A, 2B and 2X amo penicillin-resistant clinical isolates of Streptococcus pneum serotype 23F from the nasopharyngeal flora of children.";

L. Med. Microbiol. 50:828-832(2001).

R. EMBL; AF210/751; AAF17261.1; -.

R. Interpro; IPR001264; Transglycosyl.

R. Interpro; IPR001460; Transpeptdse.

R. Interpro; IPR001460; Transpeptdse.

R. Pfam; PF009912; Transglycosyl: 1.

R. Pfam; PF009912; Transglycosyl: 1.

R. Pfam; PF009125; Transglycosyl: 1.

R. Pfam; PF00905; Transglycosyl: 1.

SEQUENCE 719 AA; 79587 MW; 786EDCCBB8BCF286 CRC64;
Query Match 94.0
Best Local Similarity 92.9
Matches 619; Conservative
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-DEC-2001 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=SP 22861;
MEDLINE=21432820; PubMed=11549185;
Perron; a pactor of particular properties of particular particular particular properties of particular particula
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Streptococcus.
NCBI_TaxID=1313;
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                                  94.08;
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; Score 3274; DB 2;
; Pred. No. 5.5e-170;
31; Mismatches 16;
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SEQUENCE FROM N.A.
STRAIN-CS111 (CEPHALOSPORIN-RESISTANT CL
MEDLINE-96012191; PubMed-7574521;
Coffey T.J., Daniels M., McDougal L.K.,
Spratt B.G.;
"Genetic analysis of clinical isolates o
with high-level resistance to expanded-s
Antimicrob. Agents Chemother. 39:1306-13
EMBL; Z49095; CAA88918.1; -
                                                                                                                                                                                                                                                                                                             Q57114 PRELIMINARY;
Q57114;
01-NOV-1996 (TrEMBLTel. (
01-NOV-1996 (TrEMBLTel. (
01-JUN-2001 (TrEMBLTel. 1
                                                                                                                                                                                                                   Bacteria; Firmicutes; Streptococcus.
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Lrel. 01, Last sequence up
Lrel. 17, Last annotation
PROTEIN 1A.
                                                                                                                                                                                                                                       Bacillus/Clostridium
                      isolates of Streptococcus pneumonia
expanded-spectrum cephalosporins.";
39:1306-1313(1995).
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Q9RET6;
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01-MAY-2000
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Streptococcus
Bacteria; Fir
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InterPro; IPR001264; Transspeptdse.
InterPro; IPR001264; Transspeptdse.
Pfam; PF00912; Transg1ycosy1; 1.
Pfam; PF00905; Transg1ycosy1; 1.
ProDom; PD001895; Transg1ycosy1; 1.
ProDom; PD001895; Transg1ycosy1; 1.
SEQUENCE 719 AA; 79712 MW; 5396607C0E67D06E
                                                          PENICILLIN-BINDING
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612; Conserv
Firmicutes;
                                                        0 (TrEMBLrel. 13, 0
0 (TrEMBLrel. 13, 1
1 (TrEMBLrel. 19, 1
-BINDING PROTEIN 12
                                                                                                                                                                                                                                                                                              666
                                                                                                                                                          PRELIMINARY;
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                      pneumon
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  Bacillus/Clostridium
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Last sequence up
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Pred. No. 1.6e
33; Mismatches
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.6e-168;
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Best Local
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"Alterations to penicillin-binding proteins 1A, 2B penicillin-resistant clinical isolates of Streptoc serotype 23F from the nasopharyngeal flora of chil J. Med. Microbiol. 50:828-832(2001).

EMBL; AF210749; AAF17259.1; -

InterPro; IPR001264; Transglycosyl.
InterPro; IPR001460; Transglycosyl.
InterPro; IPR00912; Transglycosyl; 1.

Pfam; PF00905; Transglycosyl; 1.

Pfam; PF00905; Transglycosyl; 1.

ProDom; PD001895; Transglycosyl; 1.

ProDom; PD001895; Transglycosyl; 1.
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                                     STWNSPAPQQPPSTESSSSSSSSSTSQSSSTTPSTNNSTTTDPNNNTQQSNTTPDQQNQN
                                                                             AVWTGYSNRLTPIVGDGFLVAAKVYRSMITYLSEDTHPEDWTMPDGLFRNGEFVFKNGAR
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613; Conservative
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Pred. No. 1.8e
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rolates of Streptococcus p
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.8e-168;
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"Relatedness of penicillin-binding protein la geologie de l
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InterPro; IPR001266; Transpeptdse.
Pfam; PF00912; Transglycosyl; 1.
Pfam; PF00905; Transglycosyl; 1.
ProDom; PD001895; Transglycosyl; 1.
NON_TER 719 719
SEQUENCE 719 AA; 79710 MW; D90EB4
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Q54947;
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Q1-NOV-1996
Q1-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93010977; PubMed-1396576; Martin C., Sibold C., Hakenbeck R.; "Relatedness of penicillin-binding protein lactiones of penicillin-resistant Streptococcus
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Bacteria; Firmicutes; Bacillus/Clostridium
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                        clone of Streptococcus pneumoniae ar replacements of the cpsA-pbpla region Microbiology 0:00(1999).

EMBL; x67868; CAA48068.1; ---
EMBL; AF046230; AAC24695.1; ---
EMBL; AF046230; AAC34696.1; ---
EMBL; AF139883; AAD43066.1; ---
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Streptococcus pneumo
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Q54946;
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STRAIN-SP-665;
Coffey T.J., Daniels M., Enright M.C., Spratt B.G.;
"Serotype 14 variants of the Spanish ponicillin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93010977; PubMed=1396576; Martin C., Sibold C., Hakenbeck R.; Martin C. Sibold C., Hakenbeck R.; "Relatedness of penicillin-binding protein la genes from different clones of penicillin-resistant Streptococcus pneumoniae isolated in South Africa and Spain."; EMBO J. 11:3831-3836(1992).
                                                                                                                                                                                                                                                                                                                               "Association of a thr-371 substitution of penicillin-binding protein 1A with protectors pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 320-717 FROM N.A.
STRAIN-#17/Z46, #20/B98, AND #27/SHA3;
MEDLINE-98409715; PubMed-9736547;
Asahi Y., Ubukata K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 310-619 FROM N.A.
STRAIN=8303, AND 35193;
Smith A.M., Klugman K.P.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ
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VSFGINQAVETNRDWGSTMKPITDYAPALEYGYYDSTATIVHDEPYNYPGTNTPYYNWDR AVWTGYSNRLTPLYGNGLTVAAKVYRSMMTYLSEGSNPEDWNIPEGLYRNGEFVFKNGAR TGMDYYTNVDQEAQKHLWDIYNTDEYVAYPDDELQVASTIVDVSNGKVIAQLGARHQSSN SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEEETGYNLLT VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL SEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAYMDNYLKEVINQVEQETGYNLLT VYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDPYSHPEAAQDRRNLVL AVWTGYSNRLTPIVGDGFLVAAKVYRSMITYLSEDTHPEDWTMPDGLFRNGEFVFKNGAR 653 593 540 533 480 473 420 413 360 353 240 233 180 293

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ProDom; PD001895; Transqlycosyl; 1.
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nes 612; Conservative 3
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Best Local Similarity
Matches 602; Conserv
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Martin C., Sibold C., Hakenbeck R.;
Martin C., Sibold C., Hakenbeck R.;
Martin C., Sibold C., Hakenbeck R.;
Melatedness of penicillin-binding protein 1a g
clones of penicillin-resistant Streptococcus pn
South Africa and Spain.";
Submartica and Spain.";
EMBO J. 11:3831-3836(1992).
EMBL; x67870; CAA48070.1;
EMBL; x67870; CAA48070.1;
Interpro; IPR001264; Transplycosyl.
Interpro; IPR001264; Transpeptidse.
Pfam; pF00912; Transpeptidase; 1.
Pfam; pF00905; Transpeptidase; 1.
Pfam; pF00905; Transpeptidase; 1.
Pfam; pF00905; Transpeptidase; 1.
Pfam; pF00905; Transpeptidase; 1.
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01-NOV-1996 (TremBLrel. 01, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
PENICILLIN-BINDING PROTEIN 1A (FRAGMENT).
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Pred. No. 1.6e-165;
1; Mismatches 23;
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ALIGNMENTS

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AR120238
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Sequence 1 from patent US 6159469.
ARI20238
ARI20238.1 GI:14103814
                                                          1 (bases 1 to 1999)
Choi,G.H., Kunsch,C.A., Barash,S.C., Dillon,P.,
Fannon,M.R. and Rosen,C.A.
Streptococcus pneumoniae antigens and vaccines
Patent: US 6159469-A 112-DEC-2000;
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Query Match

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	960	901 TGTTTCCGTCGGAATTAACCAAGCAGTAGAAACAAACCGCGACTGGGGATCAACTATGAA 	Qу
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Fannon,M. and Dougherty.BA.
Polynucleotide of Streptococus pneumoniae and
Patent: JP 2001501833-A 145 13-FEB-2001;
HUMAN GENOME SCIENCES INC
OS Unidentified
PN JP 2001501833-A/145
PD 13-FEB-2001
13-FEB-2001
PF 30-OCT-1996 US 60/029960
PI CHARLES A KUNSCH,GIL H CHOI,PATRICK J DII
PG CHARLES A KUNSCH,GIL H CHOI,PATRICK J DII
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                                                         AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT
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2 (bases 1 to 11334) Tettelin,H., Nelson,K.E., Paulsen,I.T., Eisen,J.A., Read,T.D., Tettelin,H., Nelson,K.E., Paulsen,I.T., Haft,D.H., Dodson,R.J., Peterson,S., Heidelberg,J., DeBoy,R.T., Haft,D.H., Dodson,R.J., Durkin,A.S., Gwinn,M., Kolonay,J.F., Nelson,W.C., Peterson,J.D., Umayam,L.A., White,O., Lewis,M.R., Radune,D., Holtzapple,E., Khouri,H., Wolf,A.M., Utterback,T.R., Hansen,C.L., McDonald,L.A., Feldblyum,T.V., Angiuoli,S., Gesuwan,P., Hickey,E.K., Holt,I.E., Loftus,B.J., Uywal,M.L., Yang,F., Smith,H.O., Venter,J.C., Dougherty,B.A., Morrison,D.A., Hollingshead,S.K. and Fraser,C.M. Direct Submission Direct Submission Sibmitted (29-JUN-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA Location/Qualifiers 1. 11334 /organism="Streptococcus pneumoniae TIGR4"	Hickey,E.K., Holt,I.E., Loftus,B.J., Yang,F., Smith,H.O., Venter,J.C., Dougherty,B.A., Morrison,D.A., Hollingshead,S.K. and Fraser,C.M. Complete genome sequence of a virulent isolate of Streptococcus pneumoniae Science. 293 (5529), 498-506 (2001) 21357209 11463916	Streptococcus pneumoniae TIGR4 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae; Streptococcus. 1 (bases 1 to 11334) 1 (bases 1 to 11334) 1 (bases 1 to 1600, K.E., Paulsen, I.T., Eisen, J.A., Read, T.D., Tettelin, H., Nelson, K.E., Paulsen, I.T., Haft, D.H., Dodson, R.J., Peterson, S., Heidelberg, J., DeBoy, R.T., Haft, D.H., Dodson, R.J., Durkin, A.S., Gwinn, M., Kolonay, J.F., Nelson, W.C., Peterson, J.D., Umayam, L.A., White, O., Salzberg, S.L., Lewis, M.R., Radune, D., Holtzapple, E., Khouri, H., Wolf, A.M., Utterback, T.R., Hansen, C.L., McDonald, L.A., Feldblyum, T.V., Angiuoli, S., Dickinson, T.,	AE007349 11334 bp DNA linear BCT 31-AUG-2001 Streptococcus pneumoniae TIGR4 section 32 of 194 of the complete AE007349 AE005672 AE007349.1 GI:14971837 Streptococcus pneumoniae TIGR4.	TACCAATCCTAACAATAATACGCAACAATCAAATACAACCCCTGATCAACAAAATCAGAA 1980	TTGGAATATACCAGAGGGCTCTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTCG 7968 TTCTACGTGGAACTCACCTGCTCCACAACAACCCCCATCAACTGAAAGTTCAAGCTCATC 1860	GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT 1680
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DVSNGKVIAQLGARHQSSNVSFGINQAVETNRDWGSTWKPITDYAPALEYGVVDSTAT
IVHDEPYNYPGTNTPVYNWDRGYFGNITLQYGLQQSSWKPITDYAPALEYGVVDSTAT
IVHDEPYNYPGTNTPSDKKYCASSEKMAAAYAAFANGGTYYKPMYHKVVFS
GGSEKEFSNVGTRAMKETTAYMMTDMMKTVLTYGTGRNAYLAWLPQAGKTGTSNYTDE
EIENHIKTSQFYAPDELFAGYTRKYSMAVWTGYSNRLTPLVGKGLTVAAKVYKSMMTY
LSEGSNPEDWNIPEGLYRNGEFYFKNGARSTWNSPAPQQPPSTESSSSSSDSSTSQSS
STTPSTNNSTTYNPNNNTQQSNTTPDQQNQNPQPAQP*

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SKLVARTSSKIYDNKNQLIADLGSERVNAQANDIPTDLVKALYSIEDHRFFDHRGID
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ATKQEILTYYLIKKYYMSNGNYGMQTAAQNYYGKOLNNLSLPQLALLAGMPQAPNQYDP
YSHPEAAQDRRNLVLSEMKNQGYISAEQYEKAVNTPITDGLQSLKSASNYPAVMDNYL
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/protein_id="AAF17255.1"
/db_xref="GI:6563337"
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/transl_table=11
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Streptococcus pneumoniae
Bacteria; Firmicutes; Bac
                      GI:47419
                                 (45607)
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ponA gene f
 Bacillus/Clostridium
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                                 for
                                 DNA linear BCT 11-MAY-1995 penicillin-binding protein 1a.
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 Streptococcaceae;
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  GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA 420
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Martin,C., Sibold,C. and Hakenbeck,R. Relatedness of penicillin-binding protein la clones of penicillin-resistant Streptococcus South Africa and Spain EMBO J. 11 (11), 3831-3836 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hakenbeck, R.
Direct Submission
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/protein_id="CAA48073.1"
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1440 1598	81 AGAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACGGA 	13i 15:	. oy	
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1118	59 TGTTTCCTTCGGAATTAACCAAGCAGTAGAAACAAACCGCGACTGGGGATCAACTAT	10	о в В	
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                                                                                                                       2 (bases 1 to 2160)
Ferroni,A. and Berche
Direct Submission
Submitted (03-DEC-199
                                                                                                                                                                                                                                                                                                                                    2160 bp
Streptococcus pneumoniae isolate
1A (pbpla) gene, complete cds.
AF210746
AF210746.1 GI:6563338
                                                                                                                                                                                         Ferroni,A. and Berche,P.
Alterations to penicillin-binding proteins 1A, 2B and 2X penicillin-resistant clinical isolates of Streptococcus serotype 23F from the nasopharyngeal flora of children J. Med. Microbiol. 50 (9), 828-832 (2001)
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Streptococcus
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                                                                                                           Necker
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                                                                                              ted (03-DEC-1999) Microbiology, Hospital
-Enfants-Malades, 149 rue de Sevres, Par
Location/Qualifiers
                                             /organism="Streptococcus
/serotype="23F"
/isolate="SP 1513"
/gene="pbpla"
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                                  /db_xref="taxon:1313"
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TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAAGAACAGGCTATAACCTACTCAC
                                        ATCTGAAATGAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC
                                                                                                                                                    AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT
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TTGGAATATACCAGAGGGGCTCTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTCG
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Streptococcus pneumoniae.
Streptococcus pneumoniae
Sacteria; Firmicutes; Bac
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Relatedness of penicillin-binding protein la
clones of penicillin-resistant Streptococcus
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EMBO J. 11 (11), 3831-3836 (1992)
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IVHDKPYNPPGTNTPYYNWDRGYFGHITLQVALQOSRNVPAVETILNKVGLNRAKTFLN
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EIENHIKTSQFVAPDBLFAGYTRKYSMAVWTCYSNRLTPLVGNGLTVAAKVYRSMMTY
LSEGSNPEDMNITQGSRTYPDQNONDQDPAQP*

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/strain="63915"
/db_xref="taxon:1313"
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	TCTGCTGAACAGTATGAGAAAGCAGTCAATAC 600 CTGCTGAACAGTATGAAAAAGCAGTCAATAC 758	ATCTGAAATGAAAAATCAAGGCTACATCTV 	541 699	gb Qy
	AGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT 540	AAACCAATATGACCCCTATTCACATCCA	481 639	Dy Qy
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	TCAACTCTCACCCAACAGTTGATTAAGTTGAC 240 	TCTGCAAAGCAATTCCCTCCAAGGTGGA	181 339	ду 2У
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	ATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA 120 	TGCCCAAGCTAATGATATTCCCACAGAI	61 219	Qy Db
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Db 1179 CGTTCACGATGAGCCCTATAACTACCTGCGGACAAATACTCCTGTTTAATAACTGGGAT Db 1179 CGTTCACGATAAGCCCTATAACTACCTGGGACAAATACTCCCTGTTAATACTGGGAT Db 1179 CGTTCACGATAAGCCCTGCAACACCTGCAACACCCCTGCAACACTGCGCAACACTGCGCAACACTGCCCTGCAACACTGCCCTGCAACACTGCCCTGCAACACTGCCCTGCAACACTGCCCCTGCAACACTGCCCCAACACTGCCCCAACACTGCCCCTGCAACACTGCCCCAACACTGCCCCAACACTGCCCCAACACTGCCCCCAACACTGCCCCCAACACTGCCCCAACACTGCCCCCAACACTGCCCCCAACACTGCCCCCAACACTGCCCCCAACACTGCCCCCAACACTGCCCCCAACACTGCCCCCAACACTGCCCCCAACACTACCCCAACCGCCCCCAACACTCCCAACCGCAACACCGCCCCAACACCCCCCAACCATCCCAACCGCCCCCAACCATCCCCAACCGCCCCCAACCATCCCCAACCGCCCCCCAACCATCCCCAACCGCCCCCAACCATCCCCAACCGCCCCCCAACCATCCCCAACCGCCCCCCAACCATCCCAACCGCCCCCAACCATCCCAACCGCCCCCCAACCATCCCAACCGCAACCGCCCCCAACCCCTTTAACCACCCCCCAACCCCTTTAACCACC
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RESULT 8
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DEFINITION Sequence 2048 from Patent WO0123604.

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                 AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT
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     TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAAACAGGCTATAACCTACTCAC
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GGGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAACAATCGCGAAACGTCCCAGC CGTTCACGATGAGCCCTATAACTACCCTGGGACAAATACTCCTGTTTATAACTGGGATAG ACCGATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTAT TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT TTGGAATATACCAGAGGGGCTCTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTCG GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT GACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATACGCGTAAATATTCAAT CATGATGAAAACAGTCTTGACTTATGGAACTGGAACGAAATGCCTATCTTGCCTTGGCTCCC CGTGGAAACTCTAAACAAGGTCGGACTCAACCGCGCCAAGACTTTCCTAAATGGTCTCGG CGTGGAAACTCTAAACAAGGTCGGACTCAACCGCGCCAAGACTTTCCCTAAATGGTCTAGG AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAAACATCTGTGGGATAT TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAAACAGGCTATAACCTACTCAC GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT GACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATACGCGTAAATATTCAAT **AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAAACATCTGTGGGATAT** 1440 1320 1958 1800 1898 1740 1838 1680 1778 1620 1658 1500 1598 1538 1478 1418 1260 1358 1200 1298 1238 1080 1178 1020 1118 1058 900 998

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Nucleotide sequences of genes encoding penicillin-binding proteins from Streptococcus pneumoniae and Streptococcus oralis with high homology to Escherichia coli penicillin-binding proteins 1A and 1B J. Bacteriol. 174, 4517-4523 (1992)
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1093 a 783 c 609 g 893 t
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Similarity

99.1%; 99.4%;

Score 1981.4; Pred. No. 0;

DВ

1:

Length

Matches 1944 1824 1704 1584 1464 1404 1344 1284 1224 1164 1884 1644 1524 1104 781 721 661 601 541 481 421 361 301 241 181 121 61 _ TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA 180 1988; TGTTGATGTTTCTAACGGTAAAGTCATTGCCCAGCTAGGAGCACGCCATCAGTCAAGTAA TGTTGATGTTTCTAACGGTAAAGTCATTGCCCAGCTAGGAGCACGCCATCAGTCAAGTAA 900 TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT **AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAAACATCTGTGGGATAT** AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAAACATCTGTGGGATAT TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAAACAGGCTATAACCTACTCAC TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAAGAAACAGGCTATAACCTACTCAC ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA ATCTGAAATGAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC AAACCAATATGACCCCTATTCACATCCAGAAGCCAGCCCAAGACCGCCGAAACTTGGTCTT AAACCAATATGACCCCTATTCACATCCAGAAGCCGCCAAGACCGCCGAAACTTGGTCTT GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA AGCGATTCAGTTAGAACAAAAAGCAACCAAGCAAGAAATCTTGACCTACTATAAAATAA TTACTTTCAACTTCGACTTCCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTT TTACTTTTCAACTTCGACTTCCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTT TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA 120 Conservative 0 Mismatches 11; 0; Gaps 480 420 1223 1763 1463 1343 1283 1823 660 1703 600 1643 540 1523 360 1403 300 1943 840 1883 1583 240 780 720 0;

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Genome of the Bacterium Streptococcus pneumoniae Strain R6
J. Bacteriol. 183 (19), 5709-5717 (2001)
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2 (bases 1 to 10313)
4 (bases 1, A., Alborn, W. Jr., Arnold, J., Blaszczak, L., Burgett, Hoskins, J.A., Alborn, W., Fritz, L., Fu, D.-J., Fuller, W., Geringe Behoff, B.S., Estrem, S., Fritz, L., Fu, D.-J., Fuller, W., Geringe Gilmour, R., Glass, J.S., Hann, A., Khoja, H., Kraft, A., LaGace, R. LeBlanc, D.J., Lee, L.N., Lefkowitz, E.J., Lu, J., Matsushima, P., LeBlanc, D.J., Lee, L.N., Lefkowitz, E.J., Lu, J., Matsushima, P., McAhren, S., McHenney, M., McLeaster, K., Mundy, C., Nicas, T.I., McAhren, S., McHenney, M., McLeaster, K., Mundy, C., Nicas, T.I., Norris, F.H., O'Garra, M., Peery, R., Robertson, G.T., Rockey, P., Sun, P.-M., Winkler, M.E., Yang, Y., Young-Bellido, M., Zhao, G., Zook, C., Baltz, R.H., Jaskunas, S.R., Rosteck, P.R. Jr., Skatrud,
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Submitted (27-JUL-2001) Infectious Diseases
Company, Lilly Research Labs, Indianapolis,
Location/Qualifiers
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3871. .4274
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TFDQLNELAENFSEN"
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2932. .3459
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  /transl_table=11
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                                                                                       TAAAATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAA 2056
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ISYAQGFAQLRVASKENNWNLPFADIASIWRDGCIIRSRFLQKITDAYNRDADLANLL
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AKAPEDGKPCVTYIGPDGAGHYVKMVHNGIEYGDMQLIAESYDLMQHLLGLSAEDMAE
IFTEWNKGELDSYLIEITADILSRKDDEGQDGPIVDYILDAAGNKGTGKWTSQSSLDL
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PSSEDILLPLPLDDEEQGLDPLLLDDENPTEMTEEVEEEQNLSRLDQEDSEKKSKKGF
ILTVLALVSVIICVSAYYVYRQVARSTKEIETSQSTTANQSDVDDFNTLYDAFYTNSN
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KPVLIENLVARISAIFRGRDFIDQHCSLMKVPRTYRNLRIDVEHHTVYRGEEMIALTR
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8420. .9109
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QASSNTTSEPKPSSSNETRSSRSEVNMGLSSAGVAVQRSASRVAYNQSAIDDSNNSAW
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/gene="csrR"
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/EC_number="1.1.1.44"
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1A (pbpla) gen
AF210752
AF210752.1 GI
Alterations to penicillin-binding proteins 1A, 2B and 2) penicillin-resistant clinical isolates of Streptococcus serotype 23F from the nasopharyngeal flora of children
                         1 (bases 1 to Ferroni, A. and
                                                Streptococcus pneumoniae.
Streptococcus pneumoniae
Bacteria; Firmicutes; Bac
                                          Streptococcus.
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                                                                                                 pneumoniae isolate ne, complete cds.
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Berche, P.
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                                                 Bacillus/Clostridium
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                                                group;
                                                 Streptococcaceae;
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Ferroni,A. and Berche,P.
Direct Submission
Submitted (03-DEC-1999) M
Necker-Enfants-Malades, 1
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/db_xref="g1:653351"
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/translation="marri71262.1"
/translation="marri712021tklTyfSTSTDOTISKAQBAWLAIGLEOK
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ATKQEILTYYTIKKVYMSKGNYGKOTAAQNYYGKDLNUSLPQLALLAGMYQAPONYD
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YSHPEAAQDRRNLVLSEMKNOGYISAEQYEKAYNTPITDCLGSLKSASNYPAYMONYL
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EIEKYLKNTGYVAPDDEMFVGTTRKYAMANWTGYSNRLTPLVGDGLTVAAKVYRSMMTY
LSEGSNPEDWNIPEGLYRNGEFVFKNGARSTWSSPAPQOPPSTESSSSSSSDSTSQSN
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/serotype="23F"
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/transl_table=11
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                  AGAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACGGA
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                                                                                      Coffey,T.J., Daniels,M., Enright,M.C. and Spratt,B.G. Direct Submission
Submitted (31-MAR-1999) The Wellcome Trust Centre for the Epidemiology of Infectious Disease, Department of Zoology, University of Oxford, South Parks Road, Oxford, Oxfordshire 3PS, UK
                                                                                                                                                                              Coffey, T.J., Daniels, M., Enright, M.C. and serotype 14 variants of the Spanish penicil 9V clone of Streptococcus pneumoniae arose replacements of the cpsA-pbpla region Microbiology 145 (Pt 8), 2023-2031 (1999)
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/note="Polish variant of
Spanish serotype 9V clone
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/strain="PO-273"
                                       /serotype="14"
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busngkvlaqlgarhqasvsfgtnovavetnendgsankpitdxapaigyvsbstat
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dgskketsgnvgtrakasiskqygasekaharanggtykpmtylpagktgtstybpl
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/function="peptidoglycan
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (31-MAR-1999) The Wellcome Trust Centre for the Epidemiology of Infectious Disease, Department of Zoology, University of Oxford, South Parks Road, Oxford, Oxfordshir 3PS, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9V clone of Streptococcus pneumoniae arose replacements of the cpsA-pbpla region microbiology 145 (Pt 8), 2023-2031 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae strain
1a (pbpla) gene, complete cds.
AF139885
AF139885.1 GI:5410460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coffey, T.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99392464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coffey,T.J., Daniels,M., Enright,M.C. and Spratt,B.G. Serotype 14 variants of the Spanish penicillin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae
Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF139885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submission
/Product="penicillin-binding protein 1a"
/Product="penicillin-binding protein 
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Polish variant of the
Spanish serotype 9V clone"
1. .2160
                                                                                                                                                                                                                                                                                                                     /gene="pbpla"
/function="peptidoglycan
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                           /gene="pbpla"
1. .2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /serotype="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="PO-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                  /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:1313"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Daniels, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2160)
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PO-341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by large recombinational
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                penicillin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxfordshire
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BASE COUNT ORIGIN Query Ma Best Loc Matches 999 939 819 661 601 699 541 639 481 579 759 421 519 361 459 781 301 399 339 721 241 181 279 121 219 159 61 AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATAT TGTTGATGTTTCTAACGGTAAAGTCATTGCCCCAGCTAGGAGCACGCCATCAGTCAAGTAA TTACAATACAGACGAATACGTTGCCTATCCAGACGATGAATTGCAAGTCGCTTCTACCAT cal Similarity 1815; Conser ATCTGAAATGAAAAACCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAGTTGAC CTACAACTCCGATCAATACGTCTCTTACCCTGACGATGATTTGCAAGTCGCATCTACGGT AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT Conservative a GLGIDYPSMHYANAISSNTTESNKQYGASSEKMAAAYAAFANGGTYYKPMYIHKVVFS
DGSKKEBSNVGTRAMKETTAYMTDMMKTVLTYGTGRGAYLPHLPQAGKTGTSNYTDE
EVENHIKNTGYVAPDEMFVGYTRKYSMYGYSNRLTPIVGDGFLVAAKVYRSMMTY
LSEGSNPEDMAIPEGLYRNGEFVFKNGARSTWBSPAPQQPPSTESSSSSDSSTSQSS
STTPSTNNSTTTNNNNTQQSNTTPDQQNQNPQPAQP"

a 494 c 407 g 566 t 90 . 30 Score 1704.6; Pred. No. 0; 0; Mismatches 184; DВ 1. Indels Length 0; Gaps 420 840 878 720 818 660 600 540 638 480 578 518 360 458 998 780 758 698 300 240 338 218 60 0

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밁 QΥ B δÃ ф QΥ DЬ δõ 멍 δÃ В Qy Вb Qy Ъ δÃ 밁 δÃ 밁 Ωy В δÃ Вb δõ 망 QV В δÃ В Qy B Qy 망 δÃ В δÃ 2019 1779 1719 1479 1959 1801 1899 1839 1681 1621 1561 1659 1501 1599 1441 1539 1381 1419 1261 1359 1201 1299 1141 1239 1081 1179 1021 1119 1059 1861 961 TCAGGCTGGTAAAACAGGAACCTCTAACTATACAGACGAGGAAATTGAAAACCACATCAA ATCAGATAGTTCAACTTCACAGTCTAGCTCAACCACTCCAAGCACAAATAATAGTACGAC GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT GACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATACGCGTAAATATTCAAT AGAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACGGA TGGAACTTACTATAAACCAATGTATATCCATAAAGTCGTCTTTAGTGATGGGAGTGAAAA CAAAAAATATGGAGCAAGTAGTGAAAAGATGGCTGCTGCTTACGCTGCCTTTGCAAATGG CGTGGAAACTCTAAACAAGGTCGGACTCAACCGCCGCCAAGACTTTCCTAAATGGTCTAGG CGTTCACGATGAGCCCTATAACTACCCTGGGACAAATACTCCTGTTTATAACTGGGATAG GGCTGTATGGACAGGTTATTCGAATCGTTTAACTCCTATCGTTGGAGATGGTTTCCTAGT GAACACTGGCTATGTAGCTCCAGATGAAATGTTTGTTGGTTATACTCGTAAGTATTCTAT TAAACAATACGGAGCAAGTAGTGAAAAAATGGCTGCTTATGCTGCCTTTGCAAATGG TATCGACTATCCAAGCATGCATTATGCAAACGCCATTTCAAGTAATACAACAGAATCTAA AATCGACTACCCAAGTATTCACTACTCAAATGCCATTTCAAGTAACACAACCGAATCAGA ACCGATCACAGACTATGCTCCTGCCTTGGAGTACGGTGTCTACGATTCAACTGCTACTAT TGGCACTTACTATAAACCAATGTATATCCATAAAGTCGTCTTCAGTGATGGAAGTAAAAA GGGCTACTTTGGCAACATCACCTTGCAATACGCCCTGCAACAATCGCGAAACGTCCCAGC AGCATATTTCGGTAATATTACTCTGCAATATGCTCTTCAACAATCACGAAATGTCACAGC 1620 1718 1440 2138 2018 1860 1958 1800 1898 1838 1680 1778 1560 1658 1500 1598 1538 1298 1118

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AUTHORS
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AF139886
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ORGANISM
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ORIGIN
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Best Local S
Matches 1815
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                                     μ.
TAAAATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGCTCAA
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2 (bases 1 to 2160)
3 (bases 1 to 2160)
4 Coffey, T.J., Daniels, M., Enright, M.C. and Spratt, B.G.
5 Coffey, T.J., Daniels, M., Enright, M.C. and Spratt, B.G.
6 Coffey, T.J., Daniels, M., Enright, M.C. and Spratt, B.G.
6 Coffey, T.J., Daniels, M., Enright, M.C. and Spratt, B.G.
6 Coffey, T.J., Daniels, M.C. and Spratt, B.G.
7 Coffey, T.J., Daniels, M.C. and Spratt, B.G.
7 Coffey, T.J., Daniels, M.C. and Spratt, B.G.
7 Coffey, T.J., Daniels, M.C. and Spratt, B.G.
8 Coffey, T.J., Daniels, M.C. and Spratt, B.G.
8 Coffey, T.J., Daniels, M., Enright, M.C. and Spratt, B.G.
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8 Coffey, T.J., Daniels, M., Enright, M.C. and Spratt, B.G.
8 Coffey, T.J., Daniels, M.G.
8 Coffey, T.J., Daniels, M
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Coffey,T.J., Daniels,M., Enright,M.C. and Spratt,B.G.
Serotype 14 variants of the Spanish penicillin-resistant serotype
9V clone of Streptococcus pneumoniae arose by large recombinational
replacements of the cpsA-pbpla region
Microbiology 145 (Pt 8), 2023-2031 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF139886 2160 bp Streptococcus pneumoniae strain' 1a (pbpla) gene, complete cds. AF139886 1 GI:5410462
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                                                                                            Similarity
                                                                                                                                                                                        693
                                                                          Conservative
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                                                                                                                                                                                                                                     Spanish
1. .2160
                                                                                                                                                                                    LSEGSNPEDWNIPEGLYRNGEFVFKNGARSTWSSPAPQQPPSTESSSSSSSSSTSQSS
STTPSTNNSTTTNPNNNTQQSNTTPDQQNQNPQPAQP"
1 494 c 407 g 566 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="penicillin-binding
/protein_id="AAD43069.1"
/db_xref="GI:5410463"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:1313"
/note="Polish variant of the major
Spanish serotype 9V clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="pbpla"
/function="peptidoglycan transglycosylase-transpeptidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene⇒"pbpla"
1. .2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /serotype="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="PO-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Streptococcus
/strain="PO-342"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1/
                                                                                          90.8%;
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                                                                        0;
                                                                                          Score 1704.6;
Pred. No. 0;
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                                                                          Mismatches
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PO-342
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                                                                                                             2160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 21)
Coffey, T.J., Dania
Direct Submission
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Coffey,T.J., Daniels,M., Enright,M.C. and Spratt,B.G.
Serotype 14 variants of the Spanish penicillin-resistant serotype
9V clone of Streptococcus pneumoniae arose by large recombinational
replacements of the cpsA-pbpla region
Microbiology 145 (Pt 8), 2023-2031 (1999)
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SKLVATTSSKIYDNKNO|| IADLGSERRVUAQANID|| FDELVKA IVSLEDHREFDHRGID
SIRILGAELRNLOSUSLOGGSTITOQLIKKLTYESTSTBODTISRKAQEAWLA|| OLEOK
ATKQEILTYYINKYYMSNGNYGMQTAAQNYYGKDLNNLSLPQLALLAGMPQAPNQYDP
YSHPEAAQDRRHLULSTBMKNQGYISAEQYEKAVNFPITOEQGSLKSASNYPAYMDNYL
KEVINQVEQETGYNLLITTGMDYVTNNODEAQKHLWDIYNSDQYUSYDDDLQVASTYV
DVSNGKVIAQLGARHQASNVSFGTNQAVETNRDMGSAMKPITDYAPAIEYGVYDSTAT
MVNDLPYNYFOTISTPVYNWDRAYFGNITLQOSRNVTAVETLNKVGLDRAKTEIN
GLGIDYPSMHYANAISSNTTESNKQYGASSEKNAAAYAAFANGGTYYKBWILKYUFS
DGSKKEESNVGTRAMKETTAYMMTDMMKTVLTYGTGRGAYLPWLPOAGKTGTSNYTDE
EVENHIKNTGYVAPDEMFVQTRKYSMANWTGSNRLTPYVGDGFLVAAKVYRSMITY
LSEDTHPEDWTMPDGLFRNGEFVFKNGARSTWNSPAPQOPPSTESSSSSSDSSTSQSS
STTPSTNNSTTTNDNNNTQQSNTTPDQQNONOPQPAQP"

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/product="penicillin-binding
/protein_id="AAD43070.1"
/db_xref="GI:5410465"
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/function="peptidoglycan transglycosylase-transpeptidase"
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/note="Danish variant of the
Spanish serotype 9V clone"
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900 1058	TGTTGATGTTTCTAACGGTAAAGTCATTGCCCAGCTAGGAGCACGCCATCAGTCAG	841 999
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780 938	AACTGGGATGGATGTCTACACAAATGTAGACCAAGAAGCTCAAAAACATCTGTGGGATAT	721 879
720 878	TAATTACCTCAAGGAAGTCATCAATCAAGTTGAAGAAGAAACAGGCTATAACCTACTCAC	661 819
660 818	L ACCAATTACTGATGGACTACAAAGTCTCAAATCAGCAAGTAATTACCCTGCTTACATGGA 	601 759
600 758	LATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC	541 699
540 698	. AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT	481 639
480 638	LAGACCTCAATAATTTAAGTTTACCTCAGTTAGCCTTGCTGGCTG	421 579
420 578	GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCAGCAAAACTACTATGGTAA	361 519
360 518	. AGCGATTCAGTTAGAACAAAAAGCAACCAAGCAAGAAATCTTGACCTACTATATAAATAA	301 459

Qy	Qy	Qy	Qy	Qy	Qy	Qy	Qy	Qу	Qy	Qy
Db	Db	Db	Db	Db	Db	Db	Db	Дъ	Db	Db
1981	1921	1861	1801	1741	1681	1621	1561	150 <u>1</u>	1441	1381
2139	2079	2019	1959	1899	1839	1779	1719		1599	1539
TCCTCAACCAGCACAACCA 1999	TACCAATCCTAACAATAATACGCAACAACAATCAAATACAACCCCTGATCAACAACAATCAGAA 1980 	ATCAGATAGTTCAACTTCACAGTCTAGCTCAACCACTCCAAGCACAAATAATAGTACGAC 1920 	TTCTACGTGGAACTCACCTGCTCCACAACAACCACCCATCAACTGAAAGTTCAAGCTCATC 1860	TTGGAATATACCAGAGGGGCTCTACAGAAATGGAGAATTCGTATTTAAAAATGGTGCTCG 1800 	CGCTGCCAAAGTTTACCGCTCTATGATGACCTACCTGTCTGAAGGAAG	GGCTGTATGGACAGGCTATTCTAACCGTCTGACACCACTTGTAGGCAATGGCCTTACGGT 1680 	GACCTCTCAATTTGTAGCACCTGATGAACTATTTGCTGGCTATACGCGTAAATATTCAAT 1620 	TCAGGCTGGTAAAACAGGAACCTCTAACTATACAGACGAGGAAATTGAAAACCACATCAA 1560 	CATGATGAAAACAGTCTTGACTTATGGAACTGGACGAAATGCCTATCTTGCTTG	AGAGTTCTCTAATGTCGGAACTCGTGCCATGAAGGAAACGACAGCCTATATGATGACCGA 1440

Search completed: August 11, 2002, 03:11:46 Job time: 28792 \sec

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2: /SIDS5/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

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Copyright (c) 1993 - 2000 Compugen Ltd
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ALIGNMENTS

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AAV27323 standard; DNA;

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02-OCT-1998 AAV27323;

(first entry)

RESULT

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Choi GH, Hromockyj A, Johnson LS,
                                                                                                                                                     Streptococcus
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                                                                                                                                                                                                 Streptococcus pneumoniae SP001 nucleotide
                (HUMA-) HUMAN GENOME SCI INC.
                                 31-OCT-1996;
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                                                                                   W09818930-A2
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                                                                                                                                                       pneumoniae.
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The nucleic acid sequence encoding the Streptococcus pneumoniae protein can be useful in vaccines for inducing protective antibodies against Streptococcus pneumoniae, for treatment or prevention of infection e.g. pneumonia, otitis media or meningitis. Probes based on the nucleic acid are used to detect Streptococcus infection (by usual hybridisation or amplification methods), also for isolating Streptococcus genes or their allelic variants. The protein can be used similarly to detect specific antibodies in standard immunoassays, especially for diagnosing or monitoring infections. Antibodies which bind the protein are used to detect corresponding antigens, to purify the protein and for passive immunisation (optionally coupled to a toxin). Vaccines are administered, e.g. by injection, orally or through the skin, typically at 0.01-1000 (especially 10-300) mu g/ml per dose.
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                          atctgaaatgaaaaatcaaggctacatctctgctgaacagtatgagaaagcagtcaatac
                                     ATCTGAAATGAAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEO ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members; or (b) isolating
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                 The present sequence encodes a soluble variant of the S. pneumoniae penicillin binding protein (PBB) 1A, which lacks the 1st 38 amino acid residues of the wild type protein. Wild type PBB is a bifunctional protein, which binds the cell membrane when expressed in a bacterial cell, having transglycosylase and transpeptidase activities. The variant protein (NCIMB 4065) in conjunction with a labelled anti-bifunctional PBP monoclonal antibody, can be used to identify and assay for cpds. which bind bifunctional PBP. Such cpds., as inhibitors of bifunctional PBB have a potential use in therapeutic cpds. which inhibit the growth of antibiotic resistant bacteria. The soluble variant may also be used in X-ray crystallography.
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                                                                                                                                                                      The present invention describes a method for generating a repertory of concleic acids of tuf, fus, atpD and/or recA genes from which probes conditions are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical consecues with a combination of defined primer pairs. The method can be consecued microorganisms e.g. algae, archaea, bacteria, fungal and parasitical constants. The method can be considered microorganisms e.g. algae, archaea, bacterian, fungal and grassitical species, genus, family and group. A nucleic acid (I) contained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of any bacterium, fungus or parasite in a sample and for the consequence of the least one toxin gene. hexa nucleic acids are used for the specific and ubiquitous detection and for identification of streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against convict on the detected include Abiotrophia addacens, Bordetella sp., convictes faster results than substrate specificity or phylum or group convictes faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved.

Canahoullo to Aahoullo to Aahoullo to persent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
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cc prokaryotic cellular proliferation, their use in identifying the cg genes, their use in the discovery of novel antibiotics, the essential cc genes themselves and the encoded proteins. The prokaryote used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella cc invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. Cc and to obtain antibodies capable of binding to the expressed proteins. Cc The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen compounds of proteins of the variety of organisms. The present sequence encodes an except a vaide variety of organisms. The present sequence encodes an cc essential protaryotic cellular proliferation protein.

Cc Note: The sequence data for this patent did not form part cc format directly from WIPO at the cc format directly from WIPO at the cc format directly from WIPO at the content of the printed specification, but was obtained in electronic cc format directly from WIPO at the content of the printed specification at the content of the printed specification of the content directly from WIPO at the content directly from WIPO at the content of the printed specification in the content of the printed specification at the content of the printed specification of the content directly from WIPO at the content of the content
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23-OCT-2000;
27-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes of and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical cc species with a combination of defined primer pairs. The method can be cused for producing probes and/or primers for detecting one or more crelated microorganisms e.g. algae, archaea, bacteria, fungi and cetection and identification of an algal, archaeal, bacterial, fungi and cetection and identification of an algal, archaeal, bacterial, fungal cd and parasitical species, genus, family and group. A nucleic acid (I) cobtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the cd detection of any bacterium, fungus or parasite in a sample and for the least one toxin gene. hexA nucleic acids are used for the specific and coldiquitous detection and for identification of streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against coldiquitous detected include Abiotrophia adiacens, Bordetella sp., corynebacteriams. Microbial species or genus or family or phylum or group corynebacteriams sp., Enterobacteriaceae group, Escherichia coli, corynebacteriaceae family, Pseudomonads group, Streptococcus sp., corynebacteriaceae family, Pseudomonads group, Streptococcus sp., corynebacteriaceae family, Pseudomonads group, Escherichia coli, coli, coli, coli, coli, coli, coli, coli, col
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  Disclosure;
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The present invention describes a method for generating a repertory of CC nucleic acids of tuf, fus, atpp and/or recA genes from which probes cand/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more crelated microorganisms e.g. algae, archaea, bacteria, fungi and detection and identification of an algal, archaeal, bacterial, fungil and combination of an algal, archaeal, bacterial, fungil and comparasitical species, genus, family and group. A nucleic acid (I) comparasitical species, genus, family and group. A nucleic acid (I) comparasition of any bacterium, fungus or parasite in a sample and for the detection of any bacterium, fungus or parasite in a sample and for the comparation of any bacterium, fungus or parasite in a sample and for the comparation of any bacterium, fungus or parasite in a sample and for the comparation of any bacterium of indentification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against comparation of the detection and for identification of Streptococcus pneumoniae. (Compabacteriams, microbial species or genus or family or phylum or group comparation of the detection and include Abiotrophia adiacens, Bordetella sp., comparation of a star results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved.

Chahloolo to AAHO02304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.

Sequence 2160 B₽; 698 Α; 494 Ç 403 G; 565 Τ; 0

Query Match Best Local :

Similarity

82.2%;

DB

22;

Length

2160;

Q 밁 δÃ B B δÃ ₽ Qy Qy Ωy Qy В Дb 멍 В Ωy Вþ Qy 밁 QΥ Matches 1776; 699 541 639 481 421 519 361 459 301 399 241 339 159 181 279 121 61 1 TAAAATCTACGACAATAAAAATCAACTCATTGCTGACTTGGGTTCTGAACGCCGCGTCAA 60 ATCTGAAATGAAAATCAAGGCTACATCTCTGCTGAACAGTATGAGAAAGCAGTCAATAC TCTGCAAAGCAATTCCCTCCAAGGTGGATCAACTCTCACCCAACAGTTGATTAAGTTGAC TCGCTTCTTCGACCACAGGGGGATTGATACCATCCGTATCCTGGGAGCTTTCTTGCGCAA 180 aaaccaatatgacccctattcacatccagaagcagcccaagaccgccgaaacttggtctt AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT GGTCTACATGTCTAATGGGAACTATGGAATGCAGACAGCAGCTCAAAACTACTATGGTAA ttacttttcaacctcgacttccgaccagactatttctcgtaaggctcaggaagcttggtt TTACTTTTCAACTTCGACTTCCGACCAGACTATTTCTCGTAAGGCTCAGGAAGCTTGGTT togottottogaccacagggggattgattocatccgtatcctgggagctttcttgcgcaa tgcccaagctaatgatattcccacagatttggttaaggcaatcgtttctatcgaagacca TGCCCAAGCTAATGATATTCCCACAGATTTGGTTAAGGCAATCGTTTCTATCGAAGACCA 120 taaaatctacgacaataaaaatcaactcattgctgacttgggttctgaacgccgcgtcaa tctgcaaagtaattccctccaaggtggatcaactctcacccaacagttgattaagttgac Conservative Score 1642.2; Pred. No. 0; 0; Mismatches 0, 223; Indels 0, Gaps 218 420 600 869 638 480 578 360 458 278 758 518 300 240 0;

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The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpb and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more

e.g. algae,

or more

Disclosure;

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                                                                                                       Nucleic acid sequences are used to generate universal probes primers which can be used to identify and detect the presence archaeal, bacterial, fungal and parasitical species in a test
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Query Match
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Matches 1763;
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                                                    AAACCAATATGACCCCTATTCACATCCAGAAGCAGCCCAAGACCGCCGAAACTTGGTCTT
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RESULT
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The present invention describes a method for generating a repertory of CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes CC and/or primers are derived. The method comprises amplifying the nucleic CC acids of determined algal, archaeal, bacterial, fungal and parasitical Species with a combination of defined primer pairs. The method can be CC used for producing probes and/or primers for detecting one or more CC related microorganisms e.g. algae, archaea, bacteria, fungi and CC parasites, for universal detection and for specific and ubiquitous CC detection and identification of an algal, archaeal, bacterial, fungal CC and parasitical species, genus, family and group. A nucleic acid (I) CC obtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the detection of any bacterium, fungus or parasite in a sample and for the cast one antimicrobial agent resistance gene or at least one antimicrobial agent resistance gene or at least one toxin gene. hexA nucleic acids are used for the specific and CC ubiquitous detection and for identification of Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (I) can be used to design a therapeutic agent which is effective microorganisms. Microbial species or genus or family or phylum owhich can be detected include Abiotrophia addacens, Bordetella sy
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                                                                                                                                                                                                                                                 CC detecting an antibiotic resistant strain of Streptococcus pneumoniae CC using primers based on the penicillin binding protein 2B (pbp2B) gene CC and the pbp1B gene. The products and methods can be used for detecting CC s. pneumoniae, particularly antibiotic-resistant strains. They can be used for simultaneously diagnosing pneumonoccal meningitis and CC identifying any antibiotic-resistant S. pneumoniae strains in a sample. CC The methods can be used for detecting S. pneumoniae strains resistant CC The assays can be adapted to detect an antibiotics, preferably penicillin. CC The assays can be used to detect an antibiotic resistant strain of CC S. pneumoniae with a minimum inhibitory concentration (MIC) of CC S. pneumoniae with a minimum inhibitory concentration (MIC) of CC S. pneumoniae with a minimum inhibitory concentration are a 1043 bp and CC a 224 bp product. The present sequence represents a Streptococcus concentration penicillin transpeptidase encoding region (TER) isolate nucleotide concentration from the present invention.
                                                                     Best Local Similarity Matches 1255; Conserv
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                                                                                                              CC A polymerase chain reaction (PCR) assays have been developed for CC detecting an antibiotic resistant strain of Streptococcus pneumoniae CC using primers based on the penicillin binding protein 2B (pbp2B) gene and the pbp1A gene. The products and methods can be used for detecting CC s. pneumoniae, particularly antibiotic-resistant strains. They can be used for simultaneously diagnosing pneumococcal meningitis and CC identifying any antibiotic-resistant s. pneumoniae strains resistant CC The methods can be used for detecting S. pneumoniae strains resistant to antibiotics, e.g. beta-lactam antibiotics, preferably penicillin. CC The assays can be used to detect other pathogens causing meningitis. The assays can be used to detect an antibiotic resistant strain of CC pneumoniae with a minimum inhibitory concentration (MIC) of C 0.25-1 micro g/ml where the PCR products detected are a 1043 bp and CC 224 bp product. The present sequence represents a Streptococcus pneumoniae pbp1A transpeptidase encoding region (TER) isolate nucleotide sequence from the present invention.
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RESULT
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The present invention describes a method for generating a repertory of CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes CC and/or primers are derived. The method comprises amplifying the nucleic CC acids of determined algal, archaeal, bacterial, fungal and parasitical CC species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more CC used for producing probes and/or primers for detecting one or more CC related microorganisms e.g. algae, archaea, bacteria, fungal and CC parasites, for universal detection and for specific and ubiquitous CC detection and identification of an algal, archaeal, bacterial, fungal CC and parasitical species, genus, family and group. A nucleic acid (I) and parasition of any bacterium, fungus or parasite in a sample and for the CC detection of at least one antimicrobial agent resistance gene or at CC least one toxin gene. hexA nucleic acids are used for the specific and CC ubiquitous detection and for identification of Streptococcus pneumoniae. CC (I) can be used to design a therapeutic agent which is effective against CC which can be detected include Abiotrophia adiacens, Bordetella sp., Forberichia acid. Corynebacterium sp., Enterobacteriaceae group, Escherichia coli, Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria gonorrhoeae and Staphylococcus sp., Using DNA based tests provides faster results than substrate specificity tests as results hour and improved accuracy also achieved can

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A polymerase chain reaction (PCR) assays have been developed for detecting an antibiotic resistant strain of Streptococcus pneumoniae using primers based on the penicillin binding protein 2B (pbp2B) gene and the pbp1A gene. The products and methods can be used for detecting S. pneumoniae, particularly antibiotic-resistant strains. They can be used for simultaneously diagnosing pneumoncoccal meningitis and identifying any antibiotic-resistant S. pneumoniae strains in a sample.
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<u>gtcgtctttagtgatgggagtgaaaaagagttctctaatgtcggaactcgtgccatgaaa</u>
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                                                                                                                                                                                                                                                                                                                                                 aatacccctgtttataactgggataggggctactttggcaacatcaccttgcaatacgcc
                                                                                                                                                                                                                                                                                                                                                                   AATACTCCTGTTTATAACTGGGATAGGGGCTACTTTGGCAACATCACCTTGCAATACGCC
                                                                                                                                                                                                                                                                                                                                                                                                                      ggtgtctacgagtcaactgccactatcgttcacgatgagccctataactaccctgggaca
                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTGTCTACGATTCAACTGCTACTATCGTTCACGATGAGCCCTATAACTACCCTGGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aaccgcgactggggatcaactatgaaaccgatcacagactatgctcctgccttggagtac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACCGCGACTGGGGATCAACTATGAAACCGATCACAGACTATGCTCCTGCCTTGGAGTAC
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                                                                 CTGTCTGAAGGAAGCAATCCAGAAGATTGGAATATACCAGAGGGGCTCTACAGAAATGGA
                                                                                                                                                                                                                   GAAACGACAGCCTATATGATGACCGACATGATGAAAAACAGTCTTGACTTATGGAACTGGA
gaattcgtatttaaaaatggtgctcgttctacgtggagctcacctgctccacaacaaccc
                                                    ctgtctgaaggaagcaatccagaggattggaatataccagaggggctctacagaaatgga
                                                                                                                                                              gctggctatacgcgtaaatattcaatggctgtatggacaggctattctaaccgtctgaca
                                                                                                                                                                              GCTGGCTATACGCGTAAATATTCAATGGCTGTATGGACAGGCTATTCTAACCGTCTGACA
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